

REMARKS

In response to the office action of January 23, 2009, Applicants have amended the specification, canceled claims 6-8 and 10, and amended claims 4, 9, and 11, which when considered with the following remarks and accompanying exhibits, is deemed to place the present application in condition for allowance. Favorable consideration of all pending claims is respectfully requested.

In the January 23, 2009, office action, the Examiner has made final the restriction requirement imposed previously. Claims 1-3 and 15-28 are therefore withdrawn from consideration.

Claim 11 has been objected to as having a grammatically incorrect preamble due to it missing the word "to". As presently amended, claim 11 recites in relevant part: "the method according to..." Withdrawal of the objection is therefore warranted.

The specification has been objected to because it contains embedded hyperlinks. By this amendment, all embedded hyperlinks have been removed. Withdrawal of the objection to the disclosure is therefore respectfully requested.

Claims 4-14 have been rejected under 35 U.S.C. §112, first paragraph, as allegedly failing to comply with the written description requirement. The position of the Examiner is that the specification discloses a single species, that is, the nucleotide sequence of SEQ ID NO:1 encoding the amino acid sequence of SEQ ID NO:2, that when expressed from a seed-preferred prolamin promoter in rice plants transformed therewith, increases the harvest index of the transformed plants relative to non-transformed plants. Office Action, page 4. Solely to advance prosecution of this application, and in no way acquiescing to the position of the Examiner, Claim 4 has been amended to recite a nucleic acid molecule encoding a GRUBX protein consisting of the amino acid sequence set forth in SEQ ID NO:2. Claim 9 has been amended to recite the nucleic acid sequence SEQ ID NO:1. Applicants reserve the right to file one or more continuation applications directed to the subject matter of the claims prior to this amendment.

Applicants respectfully submit that the written description provides a number of different seed-preferred promoters for use in the present invention, prolamin being just one of them. See Table 1 of the specification (WO 2005/059147). Further, the written description also provides a number of indicia for measuring improved growth characteristics other than harvest index such as those recited in claims 12-14. See specification (WO 2005/059147) paragraph bridging pages 31 and 32.

Provided herewith at Exhibit A are data which further support the written description of the present invention insofar as the various improved growth characteristics described in the specification are quantitatively measured.

Also provided herein at Exhibit B are data measured using a seed-preferred promoter other than prolamin.

Exhibit C provides a copy of EP 1801223, which describes the PRO0058 promoter at page 15.

In view of the foregoing remarks, amendments and Exhibits, withdrawal of the rejection of claims 4-14 under the written description requirement of 35 U.S.C. 112, first paragraph, is respectfully requested.

Claims 4-14 have been rejected under 35 U.S.C. §112, first paragraph, as allegedly directed to non-enabled subject matter. According to the Examiner, the specification is enabling only for a method using the nucleotide sequence of SEQ ID NO:1 or encoding the amino acid sequence of SEQ ID NO:2. As indicated *supra*, claim 4 has been amended to recite a nucleic acid molecule encoding a GRUBX protein consisting of the amino acid sequence set forth in SEQ ID NO:2. Claim 9 has been amended to recite the nucleic acid sequence SEQ ID NO:1. Applicants reserve the right to file one or more continuation applications directed to the subject matter of the claims prior to this amendment.

In the paragraph bridging pages 6 and 7 of the office action, the Examiner posits that the specification discloses a method comprising introducing into rice plants and expressing from a seed-preferred prolamin promoter a nucleic acid molecule (SEQ ID

NO:1) encoding the amino acid sequence of SEQ ID NO:2 and “additionally discloses that transgenic plants produced by the method have an increased harvest index as compared to non-transformed control plants. Applicants repeat, reassert and incorporate by reference those remarks submitted immediately above and Exhibits A and B with respect to the specification providing a number of well known indicia for measuring improved growth characteristics other than harvest index such as those recited in claims 12-14, as well as a number of seed-preferred promoters other than prolamin. One skilled in the art having the specification of the present application in hand, would have been able to practice the presently claimed invention, without having to engage in undue experimentation. Withdrawal of the rejection of claims 4-14 under the enablement provision of 35 U.S.C. §112, first paragraph, is respectfully requested.


Claims 9 and 10, as well as claims dependent thereon, have been rejected under 35 U.S.C. §112, second paragraph, as allegedly indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. In particular, both claims 9 and 10 have been found allegedly indefinite in the recitation of “capable of hybridising” and claim 10 has been found allegedly indefinite in reciting “related gene family members. ” As claim 9 no longer recites this language, and claim 10 is canceled, withdrawal of the rejection is warranted.

Claims 4-7 and 9-10 have been rejected under 35 U.S.C. §102(b) as allegedly anticipated by Inze et al. (WO 03/085115, published October 16, 2003). The present application claims priority under section 119(e) to U.S. Provisional Application No. 60/531,866, filed December 22, 2003. Since October 16, 2003, is not more than one year prior to December 22, 2003, Inze et al. cannot be a reference under 35 U.S.C. §102(b). The following comments are made with respect to Inze et al. being treated as a section 102(a) reference. Inze has been cited for allegedly teaching a method comprising introducing and expressing or overexpressing in a plant a nucleic acid molecule isolated from *Nicotiana tabacum* that comprises the nucleotide sequence of SEQ ID NO:1 and that encodes a protein comprising the amino acids sequence of SEQ ID NO:2. Page 13, lines 23-26 and SEQ ID NO:61 of Inze et al. have been specifically cited for this teaching.

In response to the rejection, claim 4 has been amended to recite: "A method for improving plant growth characteristics, said method comprising introducing and expressing in a plant an isolated nucleic acid molecule encoding a GRUBX protein, said GRUBX protein consisting of the amino acid sequence set forth in SEQ ID NO:2." It is respectfully submitted that Inze et al. does not teach a method of improving plant characteristics via introduction and expression of a nucleic acid molecule encoding a protein consisting of the amino acid sequence set forth in SEQ ID NO:2. Withdrawal of the rejection of claims 4-7 and 9-10 is therefore respectfully requested.

In view of the foregoing remarks and amendments to the specification and claims, it is firmly believed that the present application is in condition for allowance, which action is earnestly solicited.

Respectfully submitted


Ann R. Pokalsky
Registration No.: 34,697

Dilworth & Barrese, LLP
Attorney for Applicants
1000 Woodbury Road
Woodbury, New York 11797
Tel. No. (516) 228-8484
Fax No. (516) 228-8516
ARP/ml

Annex 1

Evaluation of transgenic rice transformed with the PRO0090-CDS0669 construct

Performance of the transgenic plants of the third (T3) generation generated as described in Example 3 was evaluated in detailed following the procedures described in Example 4 of the application as filed. The T3 generation of the transgenic plants was obtained by self crossing the transgenic plants of the second generation (T2) described in Example 4 of the application as filed.

A total number of 120 *GRUBX* transformed plants were evaluated in the T3 generation, that is 40 plants per event of which 20 positives for the transgene, and 20 negatives. A total of 3 events was evaluated.

A two factor ANOVA (analysis of variants) was used as statistical model for the overall evaluation of plant phenotypic characteristics. The statistical analysis: t-test and F-test, were performed as described in the application as filed.

The results of the evaluation obtained for different biomass and seed parameters are presented in Tables 1 to 7. The transgenic plants had an overall effect of increased vegetative parameters such as plant height and Areamax and also increased seed parameters such as seed weight, thousand kernel weight, number of filled seeds, ratio number of filled seeds/total number of seeds (which is an estimation of the seed filing rate), harvest index and thousand kernel weight.

Table 1: Evaluation of the transgenic plants in T3 generation: Plant height.

Plant height					
Line	TR (pixels)	Null (pixels)	*dif	% dif	p-value
Overall effect	1084	1033	51	5.0	0.0945

* dif: Difference

Table 2: Evaluation of the transgenic plants in T3 generation: AreaMax (above ground areas of the plant).

Areamax :					
Line	TR	null	*dif	% dif	p-value
Overall effect	67251	62777	4474	7.1	0.0948

Table 3: Evaluation of the transgenic plants in T3 generation: Seed weight.

Seed weight :					
Line	TR	null	*dif	% dif	p-value
Overall effect	8.17	7.49	0.68	9.1	0.0805

Table 4: Evaluation of the transgenic plants in T3 generation: Thousand kernel weight.

Thousand kernel weight					
Line	TR	null	*dif	% dif	p-value
Overall effect	30.3	29.7	0.6	2.0	0.0191

Table 5: Evaluation of the transgenic plants in T3 generation: Harvest index.

Harvest index					
Line	TR	null	*dif	% dif	p-value
Overall effect	118.9	110.	8.1	7.4	0.1041

Table 6: Evaluation of the transgenic plants in T3 generation: Number of filled seeds.

Number of filled seeds					
Line	TR	null	*dif	% dif	p-value
Overall effect	269.2	250.0	19.1	7.7	0.1254

Table 7: Evaluation of the transgenic plants in T3 generation: Ratio number of filled seeds/ total number of seeds.

Ratio number of filled seeds/ total number of seeds					
Line	TR	null	*dif	% dif	p-value
Overall effect	73.0	67.6	5.4	8.0	0.0342

Annex 2

Evaluation of transgenic rice transformed with the PRO0058-CDS0669 construct

Cloning of the GRUBX gene of CDS0669 (described in Example 1 of the application as filed) under the control of a the PRO0058 promoter (PRO0058 is described in patent EP1801223) into a destination vector for transformation for oryza sativa was made according to the procedure of Example 2 of the application as filed to generate the PRO0058-CDS0669 construct.

Transgenic rice plants were generated with the PRO0058-CDS0669 construct according to the procedure describe din Example 3 of the application as filed.

The transgenic plants of the T2 generation were evaluated in the T2 generation according to the procedure of Example 4 of the application as filed. A total of four independent events were evaluated.

The results of the evaluation obtained for different biomass and seed parameters are presented in Tables 1 to 4.

Table 1: Evaluation of the transgenic plants in T3 generation: AreaMax (above ground areas of the plant).

Areamax :					
Line	TR	null	*dif	% dif	p-value
Overall effect	36485,00	34036,00	2448,50	7,15	0,05

Table 2: Evaluation of the transgenic plants in T3 generation: Seed weight.

Seed weight :					
Line	TR	null	*dif	% dif	p-value
Overall effect	4,38	3,64	0,74	21,45	0,04

Table 3: Evaluation of the transgenic plants in T3 generation: Harvest index.

Harvest index					
Line	TR	null	*dif	% dif	p-value
Overall effect	115,80	102,45	13,30	13,65	0,10

Table 4: Evaluation of the transgenic plants in T3 generation: Number of filled seeds.

Number of filled seeds					
Line	TR	null	*dif	% dif	p-value
Overall effect	229,10	206,05	23,05	9,00	0,04



(11) **EP 1 801 223 A2**

(12) **EUROPEAN PATENT APPLICATION**

(43) Date of publication:
27.06.2007 Bulletin 2007/26

(51) Int Cl.:
C12N 15/82 (2006.01)

(21) Application number: 07105544.6

(22) Date of filing: 04.02.2004

(84) Designated Contracting States:
AT BE BG CH CY CZ DE DK EE ES FI FR GB GR
HU IE IT LI LU MC NL PT RO SE SI SK TR

(30) Priority: 04.02.2003 EP 03075331

(62) Document number(s) of the earlier application(s) in
accordance with Art. 76 EPC:
04707946.2 / 1 532 257

(71) Applicant: CropDesign N.V.
9052 Zwijnaarde-Gent (BE)

(72) Inventors:
• Hatzfeld, Yves
59000 Lille (FR)

• Broekaert, Willem
1700 Dilbeek (BE)

(74) Representative: Mistry, Meeta
BASF AG
Global Intellectual Property, GVV/C 006
67056 Ludwigshafen (DE)

Remarks:

This application was filed on 03 - 04 - 2007 as a
divisional application to the application mentioned
under INID code 62.

(54) **Rice promoters**

(57) The present invention provides several promoters isolated from *Oryza sativa*, which promoters are capable of driving and/or regulating the expression of an operably linked nucleic acid in a plant. The expression patterns of the promoters according to the present invention have been studied in *Oryza sativa* and some of the

promoters displayed specific activity in particular cells, tissues or organs of the plant, while others displayed constitutive expression throughout substantially the whole plant. Some promoters showed weak expression, while others were strongly active.

EP 1 801 223 A2

EP 1 801 223 A2

Description

[0001] The present invention relates to the field of plant molecular biology, more particularly to nucleic acid sequences useful for driving and/or regulating expression of an operably linked nucleic acid in plants. The isolation of these nucleic acid sequences from rice, as well as their use in driving and/or regulating expression of an operably linked nucleic acid is disclosed. The present invention therefore concerns promoters, hybrid promoters, genetic constructs, expression cassettes, transformation vectors, expression vectors, host cells and transgenic plants comprising the isolated nucleic acids according to the present invention. The present invention also concerns methods for driving and/or regulating expression of a nucleic acid and methods for the production of transgenic plants.

[0002] Gene expression is dependent on initiation of transcription, which is mediated via the transcription initiation complex. Gene expression is also dependent on regulation of transcription, which regulation determines how strong, when or where a gene is expressed. Said regulation of gene expression may be mediated via transcriptional control elements, which are generally embedded in the nucleic acid sequence 5'-flanking or upstream of the expressed gene. This upstream nucleic acid region is often referred to as a "promoter" since it promotes the binding, formation and/or activation of the transcription initiation complex and therefore is capable of driving and/or regulating expression of the 3' downstream nucleic acid sequence.

[0003] Genetic engineering of plants with the aim of obtaining a useful plant phenotype, often involves heterologous gene expression, which is generally mediated by a promoter capable of driving and/or regulating expression of an operably linked heterologous nucleic acid. The phenotype of the host plant only depends on the contribution of the heterologous nucleic acid, but also on the contribution of the specific expression pattern of the chosen promoter determining how, where and when that heterologous nucleic acid is expressed. Accordingly, the choice of promoter with a suitable expression pattern is of crucial importance for obtaining the suitable phenotype. A person skilled in the art will need to have available different promoters, to determine the optimal promoter for a particular nucleic acid. For many different host plants, this availability is rather limited and there is therefore a continuing need to provide new promoters with various expression profiles.

[0004] The nucleic acids as presented in SEQ ID NO 1 to 22 were isolated from *Oryza sativa* and have been found to be capable of driving and regulating expression of an operably linked nucleic acid; their expression patterns have also been characterized. Therefore the present invention offers a collection of hitherto unknown isolated nucleic acids, which isolated nucleic acids are useful as promoters.

[0005] Accordingly, the present invention provides an isolated promoter capable of driving and/or regulating expression, comprising:

(a) an isolated nucleic acid as given in any one of SEQ ID NO 1 to 22 or the complement of any one of SEQ ID NO 1 to 22; or

(b) an isolated nucleic acid having at least 90% sequence identity with any of the DNA sequences as given in any one of SEQ ID NO 1 to 22; or

(c) an isolated nucleic acid specifically hybridizing under stringent conditions with any of the DNA sequences as given in any one of SEQ ID NO 1 to 22; or

(d) an isolated nucleic acid as defined in any one of (a) to (c), which is interrupted by an intervening sequence; or

(e) a fragment of any of the nucleic acids as defined in (a) to (d), which fragment is capable of driving and/or regulating expression.

[0006] The term "isolated" as used herein means being removed from its original source. Preferably, the "isolated" promoter is free of sequences (such as protein encoding sequences or other sequences at the 3' end) that naturally flank the promoter in the genomic DNA of the organism from which the promoter is derived. Further preferably, the "isolated" promoter is also free of sequences that naturally flank it at the 5' end. Further preferably, the "isolated" promoter may comprise less than about 5 kb, 4 kb, 3 kb, 2 kb, 1.5 kb, 1.2 kb, 1 kb, 0.8 kb, 0.5 kb or 0.1 kb of nucleotide sequences that naturally occur with the promoter in genomic DNA from the organism of which the promoter is derived.

[0007] The present invention is not limited to the nucleic acids as presented by SEQ ID NO 1 to 22. A person skilled in the art will recognize that variants or fragments of a nucleic acid may occur, whilst maintaining the same functionality. These variants or fragments may be man made (e.g. by genetic engineering) or may even occur in nature. Therefore the present invention extends to variant nucleic acids and fragments of any of SEQ ID NO 1 to 22, which variants or fragments are useful in the methods of the present invention. Such variants and fragments include:

(a) an isolated nucleic acid as given in any one of SEQ ID NO 1 to 22 or the complement of any one of SEQ ID NO 1 to 22; or

(b) an isolated nucleic acid having at least 90% sequence identity with any of the DNA sequences as given in any one of SEQ ID NO 1 to 22; or

EP 1 801 223 A2

(c) an isolated nucleic acid specifically hybridizing under stringent conditions with any of the DNA sequences as given in any one of SEQ ID NO 1 to 22; or
 (d) an isolated nucleic acid as defined in any one of (a) to (c), which is interrupted by an intervening sequence; or
 (e) a fragment of any of the nucleic acids as defined in (a) to (d), which fragment is capable of driving and/or regulating expression.

[0008] Suitable variants of any one of SEQ ID NO 1 to 22 encompass homologues which have in increasing order of preference at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity with any one of the nucleic acids as represented in SEQ ID NO 1 to 22.

[0009] The percentage of identity may be calculated using an alignment program. Preferably a pair wise global alignment program may be used, which implements the algorithm of Needleman-Wunsch (J. Mol. Biol. 48: 443-453, 1970). This algorithm maximizes the number of matches and minimizes the number of gaps. Such programs are for example GAP, Needle (EMBOSS package), stretcher (EMBOSS package) or Align X (Vector NTI suite 5.5) and may use the standard parameters (for example gap opening penalty 15 and gap extension penalty 6.66). Alternatively, a local alignment program implementing the algorithm of Smith-Waterman (Advances in Applied Mathematics 2, 482-489 (1981)) may be used. Such programs are for example Water (EMBOSS package) or matcher (EMBOSS package). "Sequence identity" as used herein is preferably calculated over the entire length of the promoters as represented by any one of SEQ ID NO 1 to 22. The length of these promoters is presented in Table 2.

[0010] Search and identification of homologous nucleic acids, would be well within the realm of a person skilled in the art. Such methods, involve screening sequence databases with the sequences provided by the present invention, for example any one of SEQ ID NO 1 to 22, preferably in a computer readable form. Useful sequence databases, include but are not limited to Genbank (<http://www.ncbi.nlm.nih.gov/web/Genbank>), the European Molecular Biology Laboratory Nucleic acid Database (EMBL) (<http://w.ebi.ac.uk/ebi-docs/embldb.html>) or versions thereof, or the MIPS database (<http://mips.gsf.de/>). Different search algorithms and software for the alignment and comparison of sequences are well known in the art. Such software includes, for example GAP, BESTFIT, BLAST, FASTA and TFASTA. Preferably BLAST software is used, which calculates percent sequence identity and performs a statistical analysis of the similarity between the sequences. The suite of programs referred to as BLAST programs has 5 different implementations: three designed for nucleotide sequence queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, Trends in Biotechnology: 76-80, 1994; Birren et al., Genome Analysis, 1: 543, 1997). The software for performing BLAST analysis is publicly available through the National Centre for Biotechnology Information.

[0011] The sequences of the genome of *Arabidopsis thaliana* and the genome of *Oryza sativa* are now available in public databases such as Genbank. Other genomes are currently being sequenced. Therefore, it is expected that as more sequences of the genomes of other plants become available, homologous promoters may be identifiable by sequence alignment with any one of SEQ ID NO 1 to SEQ ID NO 22. The skilled person will readily be able to find homologous promoters from other plant species, for example from other crop plants, such as maize. Homologous promoters from other crop plants are especially useful for practising the methods of the present invention in crop plants.

[0012] One example of homologues having at least 90% sequence identity with any one of SEQ ID NO 1 to 22 are allelic variants of any one of SEQ ID NO 1 to 22. Allelic variants are variants of the same gene occurring in two different individuals of the same species and usually allelic variants differ by slight sequence changes. Allelic variants may encompass Single Nucleotide Polymorphisms (SNPs) as well as Small Insertion/Deletion Polymorphisms (INDELs). The size of INDELs is usually less than 100 bp. SNPs and INDELs form the largest set of sequence variants in naturally occurring polymorphic strains of most organisms.

[0013] Homologues suitable for use in the methods according to the invention may readily be isolated from their source organism via the technique of PCR or hybridization. Their capability of driving and/or regulating expression may readily be determined, for example, by following the methods described in the Examples section by simply substituting the sequence used in the actual Example with the homologue.

[0014] Other suitable variants of any one of SEQ ID NO 1 to 22 encompassed by the present invention are nucleic acids specifically hybridising under stringent conditions to any one of the nucleic acids of SEQ ID NO 1 to 22. The term "hybridising" means annealing to substantially homologous complementary nucleotide sequences in a hybridization process. Tools in molecular biology relying on such a hybridization process include the polymerase chain reaction (PCR; and all methods based thereon), subtractive hybridisation, random primer extension, nuclease S1 mapping, primer extension, reverse transcription, cDNA synthesis, differential display of RNAs, and DNA sequence determination, Northern blotting (RNA blotting), Southern blotting (DNA blotting). The hybridisation process can also occur with one of the complementary nucleic acids immobilised to a matrix such as magnetic beads, Sepharose beads or any other resin. Tools in molecular biology relying on such a process include the isolation of poly (A+) mRNA. The hybridisation process can furthermore occur with one of the complementary nucleic acids immobilised to a solid support such as a nitrocellulose or nylon membrane or immobilised by e.g. photolithography to, for example, a siliceous glass support (the

EP 1 801 223 A2

latter known as nucleic acid arrays or microarrays or as nucleic acid chips). Tools in molecular biology relying on such a process include RNA and DNA gel blot analysis, colony hybridisation, plaque hybridisation, *in situ* hybridisation and microarray hybridisation. In order to allow hybridisation to occur, the nucleic acid molecules are generally thermally or chemically denatured to melt a double strand into two single strands and/or to remove hairpins or other secondary structures from single stranded nucleic acids. The stringency of hybridisation is influenced by conditions such as temperature, salt concentration and hybridisation buffer composition. Conventional hybridisation conditions are described in, for example, Sambrook (2001) Molecular Cloning: a laboratory manual, 3rd Edition Cold Spring Harbor Laboratory Press, CSH, New York, but the skilled craftsman will appreciate that numerous different hybridisation conditions can be designed in function of the known or the expected homology and/or length of the nucleic acid sequence. High stringency conditions for hybridisation include high temperature and/or low sodium/salt concentration (salts include sodium as for example in NaCl and Na₂-citrate) and/or the inclusion of formamide in the hybridisation buffer and/or lowering the concentration of compounds such as SDS (sodium dodecyl sulphate detergent) in the hybridisation buffer and/or exclusion of compounds such as dextran sulphate or polyethylene glycol (promoting molecular crowding) from the hybridisation buffer. Specifically hybridising under stringent conditions means that the sequences have to be very similar. Specific hybridization under stringent conditions is preferably carried out at a temperature of 60°C followed by washes in 0.1 to 1 XSSC, 0.1XSDS, and 1X SSC, 0.1X SDS.

[0015] The invention also relates to a nucleic acid molecule of at least 15 nucleotides in length hybridizing specifically with any of the nucleic acids of the invention. The invention also relates to a nucleic acid molecule of at least 15 nucleotides in length specifically amplifying a nucleic acid of the invention by polymerase chain reaction.

[0016] Another variant of any of SEQ ID NO 1 to 22 encompassed by the present invention are nucleic acids corresponding to any one of SEQ ID NO 1 to 22 or variants thereof as described hereinabove, which are interrupted by an intervening sequence. For example, any of the nucleic acids as presented in SEQ ID NO 1 to 22 may be interrupted by an intervening sequence. With "intervening sequences" is meant any nucleic acid or nucleotide, which disrupts another sequence. Examples of intervening sequences comprise introns, nucleic acid tags, T-DNA and mobilizable nucleic acids sequences such as transposons or nucleic acids that can be mobilized via recombination. Examples of particular transposons comprise *Ac* (activator), *Ds* (Dissociation), *Spm* (suppressor-Mutator) or *En*. The introduction of introns into promoters is now widely applied. The methods according to the present invention may also be practised using a nucleic acid sequence according to any one of SEQ ID NO 1 to 22 provided with an intron. In case the intervening sequence is an intron, alternative splice variants of the nucleic acids according to the invention may arise. The term "alternative splice variant" as used herein encompasses variants of a nucleic acid sequence in which intervening introns have been excised, replaced or added. Such splice variants may be found in nature or may be manmade. Methods for making such promoters with an intron or for making the corresponding splice variants are well known in the art.

[0017] Variants interrupted by an intervening sequence, suitable for use in the methods according to the invention may readily be determined for example by following the methods described in the Examples section by simply substituting the sequence used in the actual Example with the variant.

[0018] The variant nucleic acids as described hereinabove may be found in nature (for example allelic variants or splice variants). Additionally and/or alternatively, variants of any one of SEQ ID NO 1 to 22 as described hereinabove may be manmade via techniques well known in the art involving for example mutation, substitution, insertion, deletions or derivation. The present invention also encompasses such variants, as well as their use in the methods of the present invention.

[0019] A "mutation variant" of a nucleic acid may readily be made using recombinant DNA manipulation techniques or nucleotide synthesis. Examples of such techniques include site directed mutagenesis via M13 mutagenesis, T7-Gen *in vitro* mutagenesis (USB, Cleveland, OH), QuickChange Site Directed mutagenesis (Stratagene, San Diego, CA), PCR-mediated site-directed mutagenesis or other site-directed mutagenesis protocols. Alternatively, the nucleic acid of the present invention may be randomly mutated.

[0020] A "substitutional variant" refers to those variants in which at least one residue in the nucleic acid sequence has been removed and a different residue inserted in its place. Nucleic acid substitutions are typically of single residues, but may be clustered depending upon functional constraints placed upon the nucleic acid sequence; insertions usually are of the order of about 1 to about 10 nucleic acid residues, and deletions can range from about 1 to about 20 residues.

[0021] An "insertional variant" of a nucleic acid is a variant in which one or more nucleic acid residues are introduced into a predetermined site in that nucleic acid. Insertions may comprise 5'-terminal and/or 3'-terminal fusions as well as intra-sequence insertions of single or multiple nucleotides. Generally, insertions within the nucleic acid sequence will be smaller than 5'- or 3'-terminal fusions, of the order of about 1 to 10 residues. Examples of 5'- or 3'-terminal fusions include the coding sequences of binding domains or activation domains of a transcriptional activator as used in the yeast two-hybrid system or yeast one-hybrid system, or of phage coat proteins, (histidine)₆-tag, glutathione S-transferase-tag, protein A, maltose-binding protein, dihydrofolate reductase, Tag-100 epitope, c-myc epitope, FLAG[®]-epitope, lacZ, CMP (calmodulin-binding peptide), HA epitope, protein C epitope and VSV epitope.

[0022] The term "derivative" of a nucleic acid may comprise substitutions, and/or deletions and/or additions of naturally

EP 1 801 223 A2

and non-naturally occurring nucleic acid residues compared to the natural nucleic acid. Derivatives may, for example, comprise methylated nucleotides, or artificial nucleotides.

[0023] Also encompassed within the present invention are promoters, comprising a fragment of any of the nucleic acids as presented by any one of SEQ ID NO 1 to 22 or variants thereof as described hereinabove. A "fragment" as used herein means a portion of a nucleic acid sequence. Suitable fragments useful in the methods of the present invention are functional fragments, which retain at least one of the functional parts of the promoter and hence are still capable of driving and/or regulating expression. Examples of functional fragments of a promoter include the minimal promoter, the upstream regulatory elements, or any combination thereof.

[0024] Suitable fragments may range from at least about 20 base pairs or about 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950 or 1000 base pairs, up to about the full length sequence of the invention. These base pairs are typically immediately upstream of the transcription initiation start, but alternatively may be from anywhere in the promoter sequence.

[0025] Suitable fragments useful in the methods of the present invention may be tested for their capability of driving and/or regulating expression by standard techniques well known to the skilled person, or by the following method described in the Example section.

[0026] The promoters as disclosed in any one of SEQ ID NO 1 to 22 are isolated as nucleic acids of approximately 1.2kb from the upstream region of particular rice coding sequences (CDS). These nucleic acids may include typical elements of a promoter, which are presented in Figure 1. Generally, a promoter may comprise from coding sequence to the upstream direction: (i) an 5'UTR of pre-messenger RNA, (ii) a minimal promoter comprising the transcription initiation element (INR) and more upstream a TATA box, and (iii) may contain regulatory elements that determine the specific expression pattern of the promoter.

[0027] The term "promoter" as used herein is taken in a broad context and refers to regulatory nucleic acid sequences capable of effecting (driving and/or regulating) expression of the sequences to which they are operably linked. A "promoter" encompasses transcriptional regulatory sequences derived from a classical genomic gene. Usually a promoter comprises a TATA box, which is capable of directing the transcription initiation complex to the appropriate transcription initiation start site. However, some promoters do not have a TATA box (TATA-less promoters), but are still fully functional for driving and/or regulating expression. A promoter may additionally comprise a CCAAT box sequence and additional regulatory elements (i.e. upstream activating sequences or cis-elements such as enhancers and silencers). A "promoter" may also include the transcriptional regulatory sequences of a classical prokaryotic gene, in which case it may include a -35 box sequence and/or a -10 box transcriptional regulatory sequences.

[0028] "Driving expression" as used herein means promoting the transcription of a nucleic acid.

[0029] "Regulating expression" as used herein means influencing the level, time or place of transcription of a nucleic acid. The promoters of the present invention may thus be used to increase, decrease or change in time and/or place transcription of a nucleic acid. For example, they may be used to limit the transcription to certain cell types, tissues or organs, or during a certain period of time, or in response to certain environmental conditions.

[0030] The promoter is preferably a plant-expressible promoter. The term "plant-expressible" means being capable of regulating expression in a plant, plant cell, plant tissue and/or plant organ. Accordingly, the invention encompasses an isolated nucleic acid as mentioned above, capable of regulating transcription of an operably linked nucleic acid in a plant or in one or more particular cells, tissues or organs of a plant.

[0031] The expression pattern of the promoters according to the present invention were studied in detail and it was found that many of them were tissue-specific. Accordingly, the present invention provides "tissue-specific" promoters. The term "tissue-specific" shall be taken to indicate that expression is predominantly in a particular tissue, tissue-type, organ or any other part of the organism, albeit not necessarily exclusively in said tissue, tissue-type, organ or other part. Accordingly, the invention encompasses an isolated nucleic acid as mentioned above, capable of driving and/or regulating expression (of an operably linked nucleic acid) in a tissue-specific manner. Expression may be driven and/or regulated in the seed, embryo, scutellum, aleurone, endosperm, leaves, flower, calli, meristem, shoot meristem, discriminating centre, shoot, shoot meristem and root. In grasses the shoot meristem is located in the so-called discrimination zone from where the shoot and the leaves originate.

[0032] A tissue-specific promoter is one example of a so-called "regulated promoter". These promoters are regulated by endogenous signals such as the presence of certain transcription factors, metabolites, plant hormones, or exogenous signals, such as ageing, stresses or nutritional status. These regulations may have an effect on one or more different levels such spatial specificity or temporal specificity. Encompassed within the present invention is a nucleic acid as described hereinabove, which is a "regulated promoter". Examples of regulated promoters are cell-specific promoters, tissue-specific promoters, organ-specific promoters, cell cycle-specific promoters, inducible promoters or young tissue-specific promoters.

[0033] Alternatively and/or additionally, some promoters of the present invention display a constitutive expression pattern. Accordingly, the present invention provides a promoter as described hereinabove, which is a constitutive promoter. The term "constitutive" means having no or very few spatial or temporal regulations. The term "constitutive

EP 1 801 223 A2

expression" as used herein refers to a substantially continuously expression in substantially all tissues of the organism. The skilled craftsman will understand that a "constitutive promoter" is a promoter that is active during most, but not necessarily all, phases of growth and development of the organism and throughout most, but not necessarily all, parts of an organism.

5 [0034] The "expression pattern" of a promoter is not only influenced by the spatial and temporal aspects, but also by the level of expression. The level of expression is determined by the so-called "strength" of a promoter. Depending on the resulting expression level, a distinction is made herein between "weak" or "strong" promoters. Generally by "weak promoter" is meant a promoter that drives expression of an operably linked nucleic acid at levels of about 1/10000 transcripts to about 1/100000 transcripts to about 1/500000 transcripts. Generally, by "strong promoter" is meant a
10 promoter that drives expression at levels of about 1/10 transcripts, to about 1/100 or to about 1/1000 transcripts.

[0035] According to a particular embodiment, the invention provides an isolated promoter as mentioned hereinabove, which is a hybrid promoter. The term "hybrid promoter" as used herein refers to a chimeric promoter made, for example, synthetically, for example by genetic engineering. Preferred hybrid promoters according to the present invention comprise a part, preferably a functional part, of one of the promoters according to the present invention and at least another part,
15 preferably a functional part of a promoter. The latter part, may be a part of any promoter, including any one of the promoters according to the present invention and other promoters. One example of a hybrid promoter comprises regulatory element(s) of a promoter according to the present invention combined with the minimal promoter of another promoter. Another example of a hybrid promoter is a promoter comprising additional regulatory elements to further enhance its activity and/or to alter its spatial and/or temporal expression pattern.

20 [0036] The present invention also provides use of a functional fragment of any one of SEQ ID NO 1 to 22 or variant thereof for changing the expression pattern of a promoter. In such methods, at least part of any of the nucleic acids according to the present invention are combined with at least one fragment of another promoter.

[0037] Further, the invention provides a genetic construct comprising:

- 25 (a) An isolated promoter as defined hereinabove
(b) A heterologous nucleic acid sequence operably linked to isolated promoter of (a), and optionally
(c) A 3' transcription terminator

[0038] The term "genetic construct" as used herein means a nucleic acid made by genetic engineering.

30 [0039] The term "operably linked" to a promoter as used herein means that the transcription is driven and/or regulated by that promoter. A person skilled in the art will understand that being operably linked to a promoter preferably means that the promoter is positioned upstream (i.e. at the 5'-end) of the operably linked nucleic acid. The distance to the operably linked nucleic acid may be variable, as long as the promoter of the present invention is capable of driving and/or regulating the transcription of the operably linked nucleic acid. For example, between the promoter and the operably
35 linked nucleic acid, there might be a cloning site, an adaptor, a transcription or translation enhancer.

[0040] The operably linked nucleic acid may be any coding or non-coding nucleic acid. The operably linked nucleic acid may be in the sense or in the anti-sense direction. Typically in the case of genetic engineering of host cells, the operably linked nucleic acid is to be introduced into the host cell and is intended to change the phenotype of the host cell. Alternatively, the operably linked nucleic acid is an endogenous nucleic acid from the host cell.

40 [0041] The term "heterologous" as used herein is intended to be "heterologous to the promoter of the present invention". A nucleic acid that is heterologous to the promoter of the present invention is not naturally occurring in the nucleic acid sequences flanking the promoter of the present invention when it is in its biological genomic environment. While the nucleic acid may be heterologous to the promoter of the present invention, it may be homologous or native or heterologous or foreign to the plant host cell. The heterologous operably linked nucleic acid may be any nucleic acid (for example encoding any protein), provided that it comprises or it is flanked by at least one nucleotide which is normally not flanking
45 the promoter of the present invention.

[0042] The term "transcription terminator" as used in (c) refers to a DNA sequence at the end of a transcriptional unit which signals termination of transcription. Terminators are 3'-non-translated DNA sequences usually containing a polyadenylation signal, which facilitates the addition of polyadenylate sequences to the 3'-end of a primary transcript. Terminators active in and/or isolated from viruses, yeasts, moulds, bacteria, insects, birds, mammals and plants are known
50 and have been described in literature. Examples of terminators suitable for use in the genetic constructs of the present invention include the *Agrobacterium tumefaciens* nopaline synthase (NOS) gene terminator, the *Agrobacterium tumefaciens* octopine synthase (OCS) gene terminator sequence, the Cauliflower mosaic virus (CaMV) 35S gene terminator sequence, the *Oryza sativa* ADP-glucose pyrophosphorylase terminator sequence (t3'BT2), the *Zea mays* zein gene terminator sequence, the *rbcs-1A* gene terminator, and the *rbcs-3A* gene terminator sequences, amongst others.

55 [0043] The present invention also provides an expression cassette, a transformation vector or a plant expression vector comprising a genetic construct as described above.

[0044] An "expression cassette" as meant herein refers to a minimal genetic construct necessary for expression of a

EP 1 801 223 A2

nucleic acid. A typical expression cassette comprises a promoter-gene-terminator combination. An expression cassette may additionally comprise cloning sites, for example GatewayTM recombination sites or restriction enzyme recognition sites, to allow easy cloning of the operably linked nucleic acid or to allow the easy transfer of the expression cassette into a vector. An expression cassette may further comprise 5' untranslated regions, 3' untranslated regions, a selectable marker, transcription enhancers or translation enhancers.

[0045] With "transformation vector" is meant a genetic construct, which may be introduced in an organism by transformation and may be stably maintained in said organism. Some vectors may be maintained in for example *Escherichia coli*, *A. tumefaciens*, *Saccharomyces cerevisiae* or *Schizosaccharomyces pombe*, while others such as phagemids and cosmid vectors, may be maintained in bacteria and/or viruses. Transformation vectors may be multiplied in their host cell and may be isolated again therefrom to be transformed into another host cell. Vector sequences generally comprise a set of unique sites recognized by restriction enzymes, the multiple cloning site (MCS), wherein one or more non-vector sequence(s) can be inserted. Vector sequences may further comprise an origin of replication which is required for maintenance and/or replication in a specific host cell. Examples of origins of replication include, but are not limited to, the f1-ori and colE1.

[0046] "Expression vectors" form a subset of transformation vectors, which, by virtue of comprising the appropriate regulatory sequences, enable expression of the inserted non-vector sequence(s). Expression vectors have been described which are suitable for expression in bacteria (e.g. *E. coli*), fungi (e.g. *S. cerevisiae*, *S. pombe*, *Pichia pastoris*), insect cells (e.g. baculoviral expression vectors), animal cells (e.g. COS or CHO cells) and plant cells. One suitable expression vector according to the present invention is a plant expression vector, useful for the transformation of plant cells, the stable integration in the plant genome, the maintenance in the plant cell and the expression of the non-vector sequences in the plant cell.

[0047] Typically, a plant expression vector according to the present invention comprises a nucleic acid of any one of SEQ ID NO 1 to 22 or a variant thereof as described hereinabove, optionally operably linked to a second nucleic acid. Typically, a plant expressible vector according to the present invention, further comprises T-DNA regions for stable integration into the plant genome (for example the left border and the right border regions of the Ti plasmid).

[0048] The genetic constructs of the invention may further comprise a "selectable marker". As used herein, the term "selectable marker" includes any gene, which confers a phenotype to a cell in which it is expressed, to facilitate the identification and/or selection of cells that are transfected or transformed. Suitable markers may be selected from markers that confer antibiotic or herbicide resistance. Cells containing the genetic construct will thus survive antibiotics or herbicide concentrations that kill untransformed cells. Examples of selectable marker genes include genes conferring resistance to antibiotics (such as nptII encoding neomycin phosphotransferase capable of phosphorylating neomycin and kanamycin, or hpt encoding hygromycin phosphotransferase capable of phosphorylating hygromycin), to herbicides (for example bar which provides resistance to Basta; aroA or gox providing resistance against glyphosate), or genes that provide a metabolic trait (such as manA that allows plants to use mannose as sole carbon source). Visual marker genes result in the formation of colour (for example beta-glucuronidase, GUS), luminescence (such as luciferase) or fluorescence (Green Fluorescent Protein, GFP, and derivatives thereof). Further examples of suitable selectable marker genes include the ampicillin resistance (Amp^r), tetracycline resistance gene (Tcr), bacterial kanamycin resistance gene (Kan^r), phosphinothricin resistance gene, and the chloramphenicol acetyltransferase (CAT) gene, amongst others.

[0049] Furthermore, the present invention encompasses a host cell comprising an isolated promoter, or a genetic construct, or an expression cassette, or a transformation vector or an expression vector according to the invention as described hereinabove. In particular embodiments of the invention, the host cell is selected from bacteria, algae, fungi, yeast, plants, insect or animal host cells.

[0050] In one particular embodiment, the invention provides a transgenic plant cell comprising an isolated promoter according to the invention, or an isolated nucleic acid, or a genetic construct, or an expression cassette, or a transformation vector or an expression vector according to the invention as described hereinabove. Preferably said plant cell is a dicot plant cell or a monocot plant cell, more preferably a cell of any of the plants as mentioned herein. Preferably, in the transgenic plant cell according to the invention, the promoter or the genetic construct of the invention is stably integrated into the genome of the plant cell.

[0051] The invention also provides a method for the production of a transgenic plant, comprising:

- (a) Introducing into a plant cell an isolated promoter, for example any one of SEQ ID NO 1 to SEQ ID NO 22, or a variant or fragment thereof, or a genetic construct, or an expression cassette, or a transformation vector or an expression vector according to the present invention and as described hereinabove, and
- (b) Cultivating said plant cell under conditions promoting plant growth.

[0052] "Introducing" the above mentioned isolated promoter, or genetic construct, or expression cassette, or transformation vector or expression vector, into a host cell (e.g. plant cell) is preferably achieved by transformation. The term "transformation" as used herein encompasses the transfer of an exogenous polynucleotide into a host cell, irrespective

EP 1 801 223 A2

of the method used for transfer. In particular for plants, tissues capable of clonal propagation, whether by organogenesis or embryogenesis, are suitable to be transformed with a genetic construct of the present invention and a whole plant may be regenerated therefrom. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular plant species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g.,
5 apical meristem, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem). The polynucleotide may be transiently or stably introduced into a plant cell and may be maintained non-integrated, for example, as a plasmid. Alternatively, it may be integrated into the plant genome.

[0053] Transformation of a plant species is now a fairly routine technique. Advantageously, any of several transformation methods may be used to introduce the nucleic acids of the invention into a suitable ancestor cell. Transformation methods include the use of liposomes, electroporation, chemicals that increase free DNA uptake, injection of the DNA directly into the plant, particle gun bombardment, transformation using viruses or pollen and microprojection. Methods may be selected from the calcium/polyethylene glycol method for protoplasts (Krens, F.A. et al., 1982, Nature 296, 72-74; Negrutiu I. et al., June 1987, Plant Mol. Biol. 8, 363-373); electroporation of protoplasts (Shillito R.D. et al., 1985 Bio/
10 Technol 3, 1099-1102); microinjection into plant material (Crossway A. et al., 1986, Mol. Gen Genet 202, 179-185); DNA or RNA-coated particle bombardment (Klein T.M. et al., 1987, Nature 327, 70) infection with (non-integrative) viruses and the like. A preferred transformation method for the production of transgenic plant cells according to the present invention, is an *Agrobacterium* mediated transformation method.

[0054] Transgenic rice plants comprising any one of the promoters of the present invention are preferably produced via *Agrobacterium*-mediated transformation using any of the well-known methods for rice transformation, such as the ones described in any of the following: published European patent application EP 1198985 A1, Aldemita and Hodges (Planta, 199, 612-617, 1996); Chan et al. (Plant Mol. Biol. 22 (3) 491-506, 1993); Hiei et al. (Plant J. 6 (2) 271-282, 1994); which disclosures are incorporated by reference herein as if fully set forth. In the case of corn transformation, the preferred method is as described in either Ishida et al. (Nat. Biotechnol. 1996 Jun; 14(6): 745-50) or Frame et al. (Plant
25 Physiol. 2002 May; 129(1): 13-22), which disclosures are incorporated by reference herein as if fully set forth.

[0055] Generally after transformation, plant cells or cell groupings are selected for the presence of one or more markers which are encoded by plant-expressible genes co-transferred with the gene of interest (which could be under the control of any of the promoters of the present invention), following which the transformed material may be cultivated under conditions promoting plant growth.

[0056] The resulting transformed plant cell may then be used to regenerate a transformed plant in a manner known to persons skilled in the art. Accordingly, the method for the production of a transgenic plant as described hereinabove, may further comprise regenerating a plant from said plant cell of (a).

[0057] The present invention further provides a plant comprising a plant cell as described hereinabove. The plants may also be able to grow, or even reach maturity including for example fruit production, seed formation, seed ripening and seed setting.
35

[0058] Furthermore, progeny may be produced from these seeds, which progeny may be fertile. Alternatively or additionally, the transformed and regenerated plants may also produce progeny by non-sexual propagation such as cloning, grafting. The generated transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, a first generation (or T1) transformed plant may be selfed to give homozygous second generation (or T2) transformants, and the T2 plants further propagated through classical breeding techniques.
40

[0059] The generated transformed organisms may take a variety of forms. For example, they may be chimeras of transformed cells and non-transformed cells; clonal transformants (e.g., all cells transformed to contain the expression cassette); grafts of transformed and untransformed tissues (e.g., in plants, a transformed rootstock grafted to an untransformed scion).
45

[0060] Following DNA transfer and growth of the transformed cells, putatively transformed plant cells or plants may be evaluated, for instance using Southern analysis, for the presence of the gene of interest, copy number and/or genomic organization. Alternatively or additionally, expression levels or expression patterns of the newly introduced DNA may be undertaken using northern and/or Western analysis, both techniques being well known to persons having ordinary skill in the art.
50

[0061] The present invention clearly extends to plants obtainable by any of the methods according to the present invention, which plants comprise any of the isolated promoters or the constructs of the present invention. The present invention clearly extends to any plant parts and propagules of such plant. The present invention extends further to encompass the progeny of a primary transformed cell, tissue, organ or whole plant that has been produced by any of the aforementioned methods, the only requirement being that progeny exhibit the same genotypic and/or phenotypic characteristic(s) as those produced in the parent by the methods according to the invention. The invention also extends to harvestable parts of a plant, such as but not limited to seeds, leaves, fruits, flowers, stem cultures, stem, rhizomes, roots, tubers, bulbs and cotton fibers.
55

EP 1 801 223 A2

[0062] The term "plant" or "plants" as used herein encompasses whole plants, ancestors and progeny of plants and plant parts, including seeds, shoots, stems, roots (including tubers), and plant cells, tissues and organs. The term "plant" therefore also encompasses suspension cultures, embryos, meristematic regions, callus tissue, gametophytes, sporophytes, pollen, and microspores. Plants that are particularly useful in the methods of the invention include all plants which belong to the superfamily *Viridiplantae*, in particular monocotyledonous and dicotyledonous plants including a fodder or forage legume, ornamental plant, food crop, tree, or shrub selected from the list comprising *Acacia spp.*, *Acer spp.*, *Actinidia spp.*, *Aesculus spp.*, *Agathis australis*, *Albizia amara*, *Alsophila tricolor*, *Andropogon spp.*, *Arachis spp.*, *Areca catechu*, *Astelia fragrans*, *Astragalus cicer*, *Baikiaea plurijuga*, *Betula spp.*, *Brassica spp.*, *Bruguiera gymnorrhiza*, *Burkea africana*, *Butea frondosa*, *Cadaba farinosa*, *Calliandra spp.*, *Camellia sinensis*, *Canna indica*, *Capsicum spp.*, *Cassia spp.*, *Centroema pubescens*, *Chaenomeles spp.*, *Cinnamomum cassia*, *Coffea arabica*, *Colophospermum mopane*, *Coronilla varia*, *Cotoneaster serotina*, *Crataegus spp.*, *Cucumis spp.*, *Cupressus spp.*, *Cyathea dealbata*, *Cydonia oblonga*, *Cryptomeria japonica*, *Cymbopogon spp.*, *Cynthea dealbata*, *Cydonia oblonga*, *Dalbergia monetaria*, *Davallia divaricata*, *Desmodium spp.*, *Dicksonia squarosa*, *Diheteropogon amplexans*, *Dioclea spp.*, *Dolichos spp.*, *Dorycnium rectum*, *Echinochloa pyramidalis*, *Ehrharta spp.*, *Eleusine coracana*, *Eragrostis spp.*, *Erythrina spp.*, *Eucalyptus spp.*, *Euclea schimperi*, *Eulalia villosa*, *Fagopyrum spp.*, *Feijoa sellowiana*, *Fragaria spp.*, *Flemingia spp.*, *Freyinetia banksii*, *Geranium thunbergii*, *Ginkgo biloba*, *Glycine javanica*, *Gliricidia spp.*, *Gossypium hirsutum*, *Grevillea spp.*, *Guibourtia coleosperma*, *Hedysarum spp.*, *Hemarthria altissima*, *Heteropogon contortus*, *Hordeum vulgare*, *Hyparrhenia rufa*, *Hypericum erectum*, *Hyperthelia dissoluta*, *Indigo incarnata*, *Iris spp.*, *Leptarrhena pyrolifolia*, *Lespedeza spp.*, *Lettuca spp.*, *Leucaena leucocephala*, *Loudetia simplex*, *Lotonus bainesii*, *Lotus spp.*, *Macrotyloma axillare*, *Malus spp.*, *Manihot esculenta*, *Medicago sativa*, *Metasequoia glyptostroboides*, *Musa sapientum*, *Nicotianum spp.*, *Onobrychis spp.*, *Ornithopus spp.*, *Oryza spp.*, *Peltophorum africanum*, *Pennisetum spp.*, *Persea gratissima*, *Petunia spp.*, *Phaseolus spp.*, *Phoenix canariensis*, *Phormium cookianum*, *Photinia spp.*, *Picea glauca*, *Pinus spp.*, *Pisum sativum*, *Podocarpus totara*, *Pogonarthria fleckii*, *Pogonarthria squarrosa*, *Populus spp.*, *Prosopis cineraria*, *Pseudotsuga menziesii*, *Pterolobium stellatum*, *Pyrus communis*, *Quercus spp.*, *Rhaphiolepis umbellata*, *Rhopalostylis sapida*, *Rhus natalensis*, *Ribes grossularia*, *Ribes spp.*, *Robinia pseudoacacia*, *Rosa spp.*, *Rubus spp.*, *Salix spp.*, *Schyzachyrium sanguineum*, *Sciadopitys verticillata*, *Sequoia sempervirens*, *Sequoiadendron giganteum*, *Sorghum bicolor*, *Spinacia spp.*, *Sporobolus fimbriatus*, *Stiburus alopecuroides*, *Stylosanthes humilis*, *Tadehagi spp.*, *Taxodium distichum*, *Themeda triandra*, *Trifolium spp.*, *Triticum spp.*, *Tsuga heterophylla*, *Vaccinium spp.*, *Vicia spp.*, *Vitis vinifera*, *Watsonia pyramidata*, *Zantedeschia aethiopica*, *Zea mays*, amaranth, artichoke, asparagus, broccoli, brussel sprout, cabbage, canola, carrot, cauliflower, celery, collard greens, flax, kale, lentil, oilseed rape, okra, onion, potato, rice, soybean, straw, sugarbeet, sugar cane, sunflower, tomato, squash, and tea, trees and algae amongst others. According to a preferred feature of the present invention, the plant is a crop plant such as soybean, sunflower, canola, alfalfa, rapeseed, cotton, tomato, potato, tobacco, squash, papaya, poplar, leguminosa, flax, lupinus or sorghum. According to another preferred embodiment of the present invention the plant is a monocotyledonous plant, such as sugarcane, further preferable a cereal such as rice, maize, wheat, barley, millet, rye or oats.

[0063] The invention further provides a method for driving and/or regulating expression of a nucleic acid in a plant or plant cell, comprising:

- a) Operably linking a nucleic acid to an isolated nucleic acid according to the invention as described hereinabove, such as to any one of SEQ ID NO 1 to 22 or a variant or fragment thereof, and
- b) Introducing the resultant genetic construct into a plant or plant cell.

[0064] Preferably the operably linked nucleic acid of (a) is heterologous to the nucleic acids according to the present invention.

[0065] This method may further comprise cultivating the transformed plant or plant cell under conditions promoting growth, promoting regeneration and/or promoting maturation.

[0066] Furthermore, the expression of the operably linked nucleic acid may be driven and/or regulated in particular cells, tissues or organs of a plant. Accordingly, the invention provides a method as described above, wherein the expression is constitutive expression or tissue-specific expression. For these embodiments, reference is made to the example section where the specific expression patterns of the promoters according to the invention are described and where different types of tissue-specific expression are detailed.

[0067] The present invention further encompasses the use of an isolated nucleic acid as defined hereinabove to drive and/or regulate expression of an operably linked nucleic acid.

[0068] The person skilled in the art will recognize that provision of sequences SEQ ID NO 1 to 22, readily makes available the tools to isolate related promoters, which may have substantial sequence identity to any of SEQ ID NO 1 to 22. Additionally, provision of sequences SEQ ID NO 23 to 44 (CDS corresponding to the promoters of the present invention, see Table 1), readily makes available the tools to isolate related promoters, of which the related CDSs may have substantial sequence identity to any of SEQ ID NO 23 to 44. Therefore the present invention also encompasses

EP 1 801 223 A2

a method for isolating nucleic acids, capable of driving and/or regulating expression of an operably linked nucleic acid, comprising screening a nucleic acid sequence database to find homologues of any of the sequences represented by SEQ ID NO 1 to 22 or SEQ ID NO 23 to 44. Subsequently these homologues are used to screen a library with genomic DNA, which library is for example prepared from the organism of origin of the above mentioned homologue. The screening procedure may for example involve hybridization. Subsequently, the genomic DNA that matches the homologue, is analysed to identify the transcription initiation site and the translation initiation site of the gene corresponding to the homologue. Finally, specific primers are designed for amplification of a nucleic acid located in the region upstream (at the 5' end) of said translation initiation site.

[0069] The present invention extends to the identification of regulatory proteins that are involved in the regulation of the activity of the promoters according to the present invention. Such identification may be achieved using a yeast one-hybrid system. In such a yeast one-hybrid system the sequences according to any one of SEQ ID NO 1 to 22 are operably linked to the GAL transcription activator and transformed to a yeast cell culture. That yeast cell culture is again transformed with a library of constructs encoding candidate regulatory factors.

[0070] The present invention will now be described with reference to the following figures in which:

Figure 1 shows a general schematic representation of a promoter. Regulatory elements are sequences that may for example be responsible for special and/or temporal regulation of the promoter activity. The minimal promoter is the minimal sequence necessary and sufficient to drive expression. It includes a TATA box, which is necessary to correctly direct the RNA polymerase II to the transcription initiation site. The transcription initiation element (INR) includes the transcription initiation start site. The 5' untranslated region (5'UTR) is the region that is transcribed into pre-messenger RNA and eventually into mRNA, but is not translated into protein. The translation initiation codon is represented by the startcodon ATG.

Figure 2 is a map of the vector p4581 useful for expression in plants of a β -glucuronidase (GUS) gene under control of any one of the promoters according to the invention. This binary vector comprises a Gateway recombination cassette, suitable for the recombination cloning of any of the promoters of the present invention in front of the *Escherichia coli* β -glucuronidase (GUS) gene. This cassette contains a chloramphenicol resistance gene (CamR) and the ccdB suicide gene for counter selection of non-recombined plasmids. This GUS expression cassette further comprises the double terminator sequence T-zein and T-rbcS-deltaGA. This expression cassette is located within the left border (LB repeat, LB Ti C58) and the right border (RB repeat, RB Ti C58) of the nopaline Ti plasmid. Cloned within these borders are also selectable marker and a screenable marker genes each under control of a constitutive promoter and a terminator sequence. This vector also contains an origin of replication (pBR322) for bacterial replication and a bacterial selectable marker (Spe/SmeR) for bacterial selection.

The following figures show the results of the GUS staining of plants or plant parts transformed with the reporter vector p4581 carrying a promoter according to the present invention operably linked to the reporter gene GUS. Plants denoted "C plants" are transgenic plants grown to about 5 cm; Plants denoted "B plants" are grown to about 10 cm; and plants denoted "A plants" are grown to maturity. These A plants were used to collect different tissue samples from old leaves, young leaves and seeds.

Figure 3 shows the expression pattern of PRO0110 (RCc3, SEQ ID NO 1). GUS staining is visible in roots.

Figure 4 shows the expression pattern of PRO0005 (putative beta-amylase, SEQ ID NO 2). GUS staining is visible in seeds, more specifically in the embryo or in the scutellum of the embryo.

Figure 5 shows the expression pattern of PRO0009 (putative cellulose synthetase, SEQ ID NO 3). GUS staining is visible in roots.

Figure 6 shows the expression pattern of PRO0005 (proteinase inhibitor Rgpi9, SEQ ID NO 4). GUS staining is visible in the seeds.

Figure 7 shows the expression pattern of PRO0061 (beta expansine EXPB9, SEQ ID NO 5). GUS staining is visible in young flowers of A plants (A) and in other young expanding tissues of B plants (B) and C plants (C).

Figure 8 shows the expression pattern of PRO0063 (putative structural protein, SEQ ID NO 6). GUS staining is visible in young tissues, for example in the calli (A) or old leaves, young leaves and seeds of "A plants" (B).

Figure 9 shows the expression pattern of PRO0081 (putative caffeoyl-CoA 3-O-methyltransferase, SEQ ID NO 7). GUS staining is visible in young tissues, particularly of the shoot.

EP 1 801 223 A2

Figure 10 shows the expression pattern of PRO0091 (prolamine RP5, SEQ ID NO 8). GUS staining is visible in seeds (A), particularly in the endosperm, and in meristem (B).

5 **Figure 11** shows the expression pattern of PRO0095 (putative amino peptidase, SEQ ID NO 9). GUS staining is visible in seeds, more particularly in the embryo.

Figure 12 shows the expression pattern of PRO0111 (uclacyanin 3-like protein, SEQ ID NO 10). GUS staining is visible in roots and in meristem.

10 **Figure 13** shows the expression pattern of PRO0116 (26S proteasome regulatory particle non-ATPase subunit 11, SEQ ID NO 11). GUS staining is weakly visible in the whole plant (weak constitutive) and is particularly visible in meristem.

15 **Figure 14** shows the expression pattern of PRO0117 (putative 40S ribosomal protein, SEQ ID NO 12). GUS staining is visible in the seeds, more particularly in the endosperm.

Figure 15 shows the expression pattern of PRO0122 (chlorophyll a/b-binding protein precursor (Cab27), SEQ ID NO 13). GUS staining is visible in the shoot.

20 **Figure 16** shows the expression pattern of PRO012 (putative protochlorophyllide reductase, SEQ ID NO 14). GUS staining is visible in the shoot (above-ground tissues).

25 **Figure 17** shows the expression pattern of PRO0133 (chitinase Cht-3, SEQ ID NO 15). GUS staining is visible in the roots and meristem.

Figure 18 shows the expression pattern of PRO0151 (WS18, SEQ ID NO 16). GUS staining is visible in the calli and upper plant parts (A) as well as in the aleurone layer and embryo (B).

30 **Figure 19** shows the expression pattern of PRO0169 (aquaporine, SEQ ID NO 17). GUS staining is visible in the whole plant (constitutive expression).

35 **Figure 20** shows the expression pattern of PRO0170 (High mobility group protein, SEQ ID NO 18). GUS staining is strongly visible in the whole plant as is illustrated by the "B plants" (A), and various tissues such as old leaves, young leaves and seeds (B) and calli (C) (constitutive expression).

Figure 21 shows the expression pattern of PRO0171 (reversibly glycosylated protein RGP1, SEQ ID NO 19). GUS staining is visible in all plant parts (constitutive expression).

40 **Figure 22** shows the expression pattern of PRO0173 (cytosolic MDH, SEQ ID NO 20). GUS staining is visible in all plant parts and particularly in the shoot (above-ground tissues) and seeds.

45 **Figure 23** shows the expression pattern of PRO0175 (RAB21, SEQ ID NO 21). GUS staining is weakly visible in calli (A), meristems and young leaves, and is strongly visible in developing and maturing seeds (B) more particularly in the embryo.

Figure 24 shows the expression pattern of PRO0177 (Cdc2-1, SEQ ID NO 22). GUS staining is weakly visible in meristem and in leaf sheets.

Examples

50

[0071] The promoters according to the present invention were isolated as DNA regions spanning about 1.2 kb of the sequence upstream of the translation initiation codon (i.e. first ATG, which codon was excluded) from various rice genes. For determination of their nucleic acid sequence and their expression pattern, the following procedure was followed: First *in silico* studies on genomic rice sequences were performed. However, procedures based on automated prediction programs to locate promoter-like nucleic acid sequence are highly error prone, even for the localization the best-characterized promoter control elements such as the TATA box and the transcription initiation element (INR). Also, *in silico* determination of expression pattern is extremely speculative. Therefore, to obtain unambiguous data about the nucleic acid sequence and the expression pattern of the promoters, *in vivo* studies were performed encompassing (i) isolation

EP 1 801 223 A2

of the promoter nucleic acid sequence; (ii) operably linking a reporter gene to the promoter and introducing the resulting genetic construct into a host organisms; (iii) growing the transformed host cell under conditions allowing expression of the reporter gene, and (iv) determination of the reporter gene activity in the different tissues of the host organism. These methods are now described in more detail.

5

Example 1. Identification and isolation of the promoters**Identification of rice ESTs, the corresponding genes and their location in the rice genome**

10 [0072] Sequence databases, comprising rice sequences, were searched for rice expressed sequence tags (ESTs). Subsequently an *"in silico"* Northern-blot was performed to allow identification of EST families that are strongly expressed or that are specific for a particular organ. This analysis included normalization of the numbers of ESTs isolated from different plant organs. The ESTs families with an interesting distribution among source cDNA libraries were selected for further analysis and sequence homology searches. After sequence homology searches in combination with scanning
15 scientific data, the genes that correspond to those families of ESTs were identified from sequence databases and a (putative) function and corresponding gene name was given (see Table 1). Subsequently, the corresponding promoter region was isolated by the following procedure. In a first step the TIGR database was searched to find a tentative contig corresponding to an EST family. Sequence homology was found using standard computer programs, such as Blast N using standard parameters (typically G Cost to open a gap = 5, E Cost to extend a gap = 2, q Penalty for a mismatch
20 in the blast portion of run = -3, r Reward for a match in the blast portion of run = 1, e Expectation value = 10.0, W Word size = 11, v Number of one-line descriptions = 100, b Number of alignments to show = 100, Matrix = BLOSUM62). The TIGR database (The Institute for Genomic Research), provides Tentative Contigs (TC) which are sequence predictions based on contig building from all known EST, from all known cDNA and from reconstructed mRNA. The TCs used for identification of the promoters of the present invention are represented in Table 1. In a second step these TCs were
25 used to locate the corresponding gene on a genomic sequence, which gene comprises the coding region as well as the promoter region. Generally, these genomic sequences were BAC clones, which are represented herein by their Genbank accession number (see Table 1). From these BAC clones the sequence identity of the promoter region could be determined.

30 [0073] Table 1: list of rice promoters of the present invention. The promoter sequences are represented herein by their SEQ ID NO and promoter number (PRO). The coding sequences (CDS) naturally driven by a promoter of the present invention are represented by their name, by SEQ ID NO and by Tentative contig (TC) accession number of the TIGR database. The Genomic sequences (BAC clones or genes) comprising a promoter region of the present invention are represented by their Genbank accession number.

Prom SEQ ID NO	Prom number	CDS name	CDS SEQ ID NO	CDS TC	BAC clone (*or gene)
1	PRO0110	RCc3	23	TC89946	AC037426
2	PRO0005	putative beta-amylase	24	TC90358	AC022457
3	PRO0009	putative cellulose synthase	25	TC83635	AC022457
4	PRO0058	proteinase inhibitor Rgpi9	26	TC83117	AF044059
5	PRO0061	beta expansine EXPB9	27	TC89913	AC020666
6	PRO0063	structural protein	28	TC89985	AP001278
7	PRO0081	putative caffeoyl-CoA 3-O-methyltransferase	29	TC89891	AP000364
8	PRO0091	prolamine RP5	30	TC89670	AF156714*
9	PRO0095	putative methionine aminopeptidase	31	TC89883	AC027133

EP 1 801 223 A2

(continued)

Prom SEQ ID NO	Prom number	CDS name	CDS SEQ ID NO	CDS TC	BAC clone (*or gene)
10	PRO0111	uclacyanin 3-like protein	32	TC90434	AJ307662
11	PRO0116	26S proteasome regulatory particle non-ATPase subunit 11	33	TC83072	AP000969
12	PRO0117	putative 40S ribosomal protein	34	TC90038	AC090871
13	PRO0122	chlorophyll a/b-binding protein presursor (Cab27)	35	TC82936	AP004700
14	PRO0123	putative protochlorophyllide reductase	36	TC89839	AL606456
15	PRO0133	chitinase Cht-3	37	TC85888	D16223*
16	PRO0151	WSI18	38	TC84300	AP003023
17	PRO0169	aquaporine	39	TC89687	AP005108
18	PRO0170	High mobility group protein	40	TC89846	AP004004
19	PRO0171	reversibly glycosylated protein RGP1	41	TC82935	AC090874
20	PRO0173	cytosolic MDH	42	TC82977	AC037425
21	PRO0175	RAB21	43	TC83646	Y00842*
22	PRO0177	Cdc2-1	44	TC90619	AP004765

Identification and Isolation of the promoter regions of rice genes

[0074] Starting from the sequence information of the genes and their location in the rice genome, the promoter regions of these genes were isolated as the DNA region spanning about 1.2 kb upstream of the translation initiation codon (i.e. first ATG), which codon was excluded. When an intervening sequence such as an intron, was present in the 5' untranslated region of the gene, the isolated DNA region was taken as the region spanning about 1.2 kb plus the length of that intervening sequence. The promoter regions were isolated from genomic DNA of *Oryza sativa Japonica* or exceptionally from *Oryza sativa Indica* via PCR using specific primers. These specific primers comprise AttB recombination sites, suitable for recombination cloning of the isolated promoter region. These specific primers are herein represented as SEQ ID NO 45 to 88 and are listed in Table 2. Conditions for PCR were as follows: 1 cycle of 2 min at 94°C, 35 cycles of 1 min at 94°C, 1 min at 58°C and 2 min at 68°C, and 1 cycle of 5 min at 68°C. The length of the expected PCR fragment is also indicated in Table 2. The corresponding PCR fragment was purified from the PCR reaction mix via gele electrophoresis and subsequent purification using Zymoclean Gel DNA Recovery Kit (Zymo Research, Orange, California).

Table 2: Overview of the primers used to isolate the rice promoters of the present invention and the length of the rice promoter regions.

Promoter SEQ ID NO	Promoter number	Prom length	Primer forward SEQ ID NO	Primer forward	Primer reverse SEQ ID NO	Primer reverse
1	PRO0110	1264	45	prm3780	67	prm3781

EP 1 801 223 A2

(continued)

Promoter SEQ ID NO	Promoter number	Prom length	Primer forward SEQ ID NO	Primer forward	Primer reverse SEQ ID NO	Primer reverse
2	PRO0005	1215	46	prm2768	68	prm2769
3	PRO0009	1038	47	prm2420	69	prm2421
4	PRO0058	1301	48	prm2853	70	prm2854
5	PRO0061	1243	49	prm2426	71	prm2427
6	PRO0063	1019	50	prm2855	72	prm2856
7	PRO0081	1212	51	prm3025	73	prm3026
8	PRO0091	1052	52	prm3029	74	prm3030
9	PRO0095	1216	53	prm3061	75	prm3062
10	PRO0111	1237	54	prm3031	76	prm3032
11	PRO0116	1100	55	prm3051	77	prm3052
12	PRO0117	1216	56	prm3592	78	prm3049
13	PRO0122	1210	57	prm5131	79	prm2195
14	PRO0123	123	58	prm3782	80	prm2197
15	PRO0133	1808	59	prm2844	81	prm2845
16	PRO0151	1828	60	prm2973	82	prm2974
17	PRO0169	1267	61	prm3770	83	prm3771
18	PRO0170	1130	62	prm3772	84	prm3773
19	PRO0171	1230	63	prm3774	85	prm3775
20	PRO0173	1234	64	prm3776	86	prm3777
21	PRO0175	1553	65	prm3800	87	prm3801
22	PRO0177	1087	66	prm5135	88	prm5136

Example 2. Cloning of promoter-GUS reporter vectors for plant transformation

[0075] The purified PCR fragments of Example 1, corresponding to the promoter regions of the present invention, were cloned into the pDONR201 entry plasmid of the Gateway™ system (Life Technologies) using the "BP recombination reaction". The identity and base pair composition of the cloned insert was confirmed by sequencing and additionally, the resulting plasmid was tested via restriction digests.

[0076] In order to clone each of the promoters of the present invention in front of a reporter gene, each entry clone of Example 1 was subsequently used in an "LR recombination reaction" (Gateway™) with the destination vector p4581. This destination vector was designed to operably link each promoter of the present invention to the *Escherichia coli* beta-glucuronidase (GUS) gene via the substitution of the Gateway recombination cassette in front of the GUS gene. Furthermore this destination vector is suitable for transformation of plants and comprises within the T-DNA left and right borders the resulting promoter-GUS cassette and selectable marker and screenable marker cassettes (see Figure 2). The resulting reporter vectors, comprising a promoter of the present invention operably linked to GUS, are subsequently transformed into *Agrobacterium* strain LBA4044 and subsequently into rice plants using standard transformation techniques.

Example 3. Expression patterns of the promoter-GUS reporter cassette in plants Growth and harvest of transgenic plants or plant parts at various stages (C plants, B plants and A plants)

[0077] For each promoter-GUS reporter construct, 3 T0 transgenic rice plants were generated from transformed cells. Plant growth was performed under normal conditions. The first transgenic plant was sacrificed for GUS staining when

EP 1 801 223 A2

it had reached a size of about 5 cm, which plant is named herein "C plant". The second transgenic plant was sacrificed for GUS staining when it had reached a size of about 10 cm, which plant is named herein "B plant". The third transgenic plant was kept for seed production and is named herein "A plant". GUS staining was performed on complete C and B plants. On A plants, GUS staining was performed on leaf pieces, flowers and section of seeds at various developmental stages. A plants were allowed to set seed, which seeds were used after harvest for confirmation of the expression pattern in T1 plants.

GUS staining

[0078] The sacrificed plants or plant parts were covered with 90% ice-cold acetone and incubated for 30 min at 4 °C. After 3 washes of 5 min with Tris buffer [15,76 g Trizma HCl (Sigma T3253) + 2,922 g NaCl in 1 l bid, adjusted to pH 7,0 with NaOH], the material was covered by a Tris/ferricyanate/X-Gluc solution [9,8 ml Tris buffer + 0,2 ml ferricyanate stock (0,33 g Potassium ferricyanate (Sigma P3667) in 10 ml Tris buffer)+ 0,2 ml X-Gluc stock (26,1 mg X-Gluc (Europa Bioproducts ML 113A) in 500 µl DMSO)]. Vacuum infiltration was applied for 15 to 30 minutes. The plants or plant parts were incubated for up to 16 hours at 37 °C until development of blue colour was visible. The samples were washed 3 times for 5 minutes with Tris buffer. Chlorophyll was extracted in ethanol series of 50%, 70% and 90% (each for 30 minutes).

Expression patterns of the promoters of the present invention

[0079] The expression patterns of the rice promoters of the present invention are summarized in Table 3.

Table 3: expression patterns of the rice promoters of the present invention

PRO SEQ ID NO	Promoter number	Promoter name	Expression pattern
1	PRO0110	RCc3	strong root
2	PRO0005	putative beta-amylase	Embryo (scutellum)
3	PRO0009	putative cellulose synthase	weak in roots
4	PRO0058	proteinase inhibitor Rgpi9	seed
5	PRO0061	beta expansine EXPB9	weak in young tissues
6	PRO0063	structural protein	young tissues+calli+embryo
7	PRO0081	putative caffeoyl-CoA 3-O-methyltransferase	shoot
8	PRO0091	prolamine RP5	meristem + strong in endosperm
9	PRO0095	putative methionine aminopeptidase	embryo
10	PRO0111	uclacyanin 3-like protein	weak meristem
11	PRO0116	26S proteasome reg. particle non-ATPase s.u. 11	weak meristem
12	PRO0117	putative 40S ribosomal protein	weak in endosperm
13	PRO0122	chlorophyll a/b-binding protein presursor (Cab27)	weak in shoot
14	PRO0123	putative protochlorophyllide reductase	strong shoot specific
15	PRO0133	chitinase Cht-3	weak meristem specific
16	PRO0151	WS118	Calli + shoot + strong embryo
17	PRO0169	aquaporine	medium constitutive
18	PRO0170	High mobility group protein	strong constitutive
19	PRO0171	reversibly glycosylated protein RGP1	weak constitutive
20	PRO0173	cytosolic MDH	Shoot and seed

EP 1 801 223 A2

(continued)

PRO SEQ ID NO	Promoter number	Promoter name	Expression pattern
21	PRO0175	RAB21	embryo
22	PRO0177	Cdc2-1	weak in meristem + strong seed

[0080] The following paragraphs describe the observed expression patterns of the promoters of the present invention in more detail. The observations are based on the visual inspection of the GUS stained tissues as described above. It is to be understood that for some promoters expression may be weak and that expression in certain tissues may only be visible with very sensitive detection methods.

PRO0110 - SEQ ID NO 1-RCc3

[0081] 1 construct (OS1432), which is a reporter vector as described in Example 2 comprising PRO0110 was investigated. 25 calli, 14 C, 21 B plants and 21 A plants were analysed. There was no expression visible in calli, but strong expression in roots of C plants (93%) and of B plants (81 %) was observed. No expression in the shoots of A plants was observed. Therefore the RCc3 promoter PRO0110 is suitable for strong expression in roots.

PRO0005 - SEQ ID NO 2 - putative beta-amylase

[0082] 1 construct (OS1365) was investigated. 28 calli, 24 B plants and 22 A plants were analysed. Occasional expression in calli (7%) was observed as well as occasional weak expression in roots (4%) and shoots (12%) of B plants, expression in the scutellum of embryos of A plants (43%) and occasional expression in leaves (5%) of A plants. This promoter is therefore suitable for expression in embryo, more preferably in the scutellum of the embryo. This region of the embryo is also referred to as the transfer layer of the embryo. This promoter may have some leakiness in other tissues.

PRO0009 - SEQ ID NO 3- putative cellulose synthase

[0083] 1 construct (OS1461) was investigated. 20 calli, 20 C, 20 B plants and 20 A plants were analysed. Occasional expression in calli (20 %) was observed as well as weak expression in roots (55%) of C plants, occasional expression in young leaves (10%) of C plants and weak expression in the roots (25%) of B plants. No expression in leaves of A or B plants was observed. Therefore this promoter is suitable for expression in roots. This promoter may show some leakiness in the leaves.

PRO0058 - SEQ ID NO 4- proteinase inhibitor Rgpi9

[0084] 1 construct (OS1370) was investigated. 13 B plants and 12 A plants were analysed. No expression was observed in B plants. In A plants, no expression was observed in the leaves, but there was strong expression in endosperm and embryo (58-42%). Therefore, this promoter PRO0058 is suitable for expression in seeds.

PRO0061 - SEQ ID NO 5- beta expansine EXPB9

[0085] 2 constructs (OS1441 and OS1460) were investigated. 20 calli, 32 C, 32 B plants and 32 A plants were analysed. Weak expression was observed in the leaves of C and B plants. In A plants expression in the flowers was observed (44%), more particularly in lemma of young spikelets. It was concluded that the promoter PRO0061 is suitable for expression in young tissue, more preferably in young, developing or expanding tissue, more preferably in green tissue.

PRO0063 - SEQ ID NO 6- putative structural protein

[0086] 1 construct (OS1446) was investigated. 13 calli, 13 C, 13 B plants and 12 A plants were analysed. In calli, weak expression was detected (92%). In C plants, there was no expression in roots and there was weak expression in some leaves (46%). In B plants, there was no expression in roots and weak expression in young tillers (78%) or young leaves (54%), but no expression in old leaves. In A plants, there was occasional expression in young leaves (17%) and expression in embryo and scutellum (42%). Therefore it was concluded that this promoter is active in the above-ground tissues, such as leaf, stem and seed. These data demonstrate that the promoter is suitable for expression in calli and in the shoot, and for expression in young tissues and seeds.

EP 1 801 223 A2***PRO0081 - SEQ ID NO 7- putative caffeoyl-CoA 3-O-methyltransferase***

[0087] 1 construct (OS1419) was investigated. 20 calli, 20 C, 20 B plants and 20 A plants were analysed. No expression was observed in Calli. Expression was observed in C plants, more particularly weak expression in root cylinder (40%) and weak expression in young leaves (80%) and in old leaves. Expression was also observed in B plants, more particularly weak expression in roots (25%) and weak expression in young leaves (80%). Expression was also observed in young leaves (50%) of A plants. It was concluded that promoter PRO0081 is suitable for expression in above-ground tissues, preferably in the shoot. This promoter may have some leakage of expression in roots.

PRO0091 - SEQ ID NO 8- prolamine RP5

[0088] 1 construct (OS1558) was investigated. 12 C, 12 B plants and 12 A plants were analysed. Weak expression was observed in the discrimination centre (50%) of C plants and in the discrimination centre (58%) of B plants. Strong expression was observed in endosperm (55%) of A plants. This promoter was found to be useful for strong expression in the endosperm, with leakiness in meristem, preferably the shoot meristem or discrimination centre.

PRO0095 - SEQ ID NO 9- putative methionine aminopeptidase

[0089] 1 construct (OS1423) was investigated. 16 calli, 14 C, 14 B plants and 16 A plants were analysed. Some expression was observed in root-tips (36 %) of C plants and in the embryo (38%) of A plants, but not in endosperm of A plants. It was concluded that PRO0095 is suitable for expression in embryo.

PRO0111 - SEQ ID NO 10- uclacyanin 3-like protein

[0090] 1 construct (OS1421) was investigated. 22 calli, 21 C, 22 B plants and 21 A plants were analysed. Weak expression was observed in the discrimination centre and meristems (77%) of B plants. It was concluded that promoter PRO0111 is suitable for weak expression in the meristem, preferably in shoot meristem or discrimination centre.

PRO0116 - SEQ ID NO 11-26S proteasome regulatory particle non-A TPase subunit 11

[0091] 1 construct (OS1679) was investigated. 13 C, 14 B plants and A plants were analysed. Weak expression was observed in meristem/discrimination centre of C plants (38%) and of B plants (71%) and in young leaf sheaths of C plants (77%) and of B plants (21%). It was concluded that promoter PRO0116 is suitable for expression in meristem, preferably in shoot meristem or discrimination centre.

PRO0117- SEQ ID NO 12- putative 40S ribosomal protein

[0092] 1 construct (OS1425) was investigated. 9 calli, 9 C, 9 B plants and 9 A plants were analysed. Occasional weak expression was observed in roots (22%) and in young leaf blades (44%) of C plants. Expression was mainly observed in endosperm (37%) of A plants. Therefore, promoter PRO117 was found to be suitable for expression in endosperm and may have some leakiness in young leaves.

PRO0122 - SEQ ID NO 13- chlorophyll a/b-binding protein precursor (Cab27)

[0093] 1 construct (OS1675) was investigated. 38 calli, 38 C, 38 B plants and 15 A plants were analysed. Very weak expression was observed in the discrimination centre and young leaf sheaths of C plants. It was concluded that this promoter PRO0122 is suitable for weak expression in shoots.

PRO0123 - SEQ ID NO 14- putative protochlorophyllide reductase

[0094] 1 construct (OS1433) was investigated. 21 calli, 18 C, 19 B plants and 18 A plants were analysed. Strong expression was observed in shoots (33-68%) of C plants and B plants (63-79%). In B plants there was also occasional expression in roots. In A plants, again strong expression in young leaves (73%) was observed, as well as occasional expression in old leaves (39%). It was concluded that this promoter is suitable for strong expression in shoots, preferably in leaves.

EP 1 801 223 A2**PRO0133 - SEQ ID NO 15- chitinase Cht-3**

[0095] 1 construct (OS1687) was investigated. 15 calli, 12 C, 16 B plants and 12 A plants were analysed. Weak expression was observed in calli (66%) and in the discrimination centre/meristem (50%) of B plants. It was concluded that promoter PRO0133 is suitable for weak expression in meristem, preferably in shoot meristem or discrimination centre.

PRO0151 - SEQ ID NO 16- WSI18

[0096] 1 construct (OS1458) was investigated. 22 calli, 16 C, 16 B plants and 13 A plants were analysed. Strong expression was observed in calli (91 %) and weak expression in shoots of C plants (62%). In A plants there was very strong expression in the aleurone layer and in the embryo (46%). It was concluded that promoter PRO0151 is suitable for strong expression in calli and in seeds, more particularly in the aleurone layer and in the embryo of the seeds.

PRO0169 - SEQ ID NO 17- aquaporine

[0097] 1 construct (OS1911) was investigated. 11 calli, 10 C plants, B plants and A plants were analysed. Some expression (55%) was observed in calli and in roots (30%) of C plants. Furthermore, good expression was observed in shoot tissues (80%) of C plants and in young leaves of B plants. It was concluded that this promoter is suitable for constitutive expression, preferably constitutive in young plants.

PRO0170 - SEQ ID NO 18- High mobility group protein

[0098] 1 construct (OS1434) was investigated. 23 calli, 21 C, 21 B plants and 14 A plants were analysed. Expression was observed in calli (52%) and in roots (51%) of C plants. Moreover, strong expression was observed in young leaves (81%) of C plants, in roots (86%) of B plants and in young leaves (86%) of B plants. In A plants there was strong expression in young leaves (75%), old leaves (43%), embryo and aleurone but a weaker expression in endosperm (82%). It was concluded that promoter PRO0170 is suitable for strong constitutive expression.

PRO0171 - SEQ ID NO 19- reversibly glycosylated protein RGP1

[0099] 1 construct (OS1762) was investigated. 18 calli, 11 C and 13 B plants were analysed. Strong expression was observed in calli (44%) and in all tissues (27%) of C plants. In all tissues of B plants (16%), expression was somewhat weaker but most pronounced the in discrimination centres (46%). It was concluded that promoter PRO0171 is suitable for constitutive expression.

PRO0173 - SEQ ID NO 20- cytosolic MDH

[0100] 1 construct (OS1435) was investigated. 17 calli, 17 C, 17 B plants and 15 A plants were analysed. Occasional expression (12%) was observed in calli and weak expression was observed in upper parts (24-69%) of C plants as well as in young leaves (41 %) of B plants. In A plants, expression in leaves (33%) was observed and strong expression in seeds (38%), but not in the root. It was concluded that the promoter PRO0173 is suitable for expression in above-ground tissues especially for constitutive expression in the shoot and especially in the seeds.

PRO0175 - SEQ ID NO 21- RAB21

[0101] 1 construct (OS1436) was investigated. 16 calli, 12 C, 15 B plants and 15 A plants were analysed. Expression was observed in some calli (31 %), in the discrimination centres (42%) of C plants and in young leaves (25-58%) of C plants and A plants(15 %). Furthermore, very strong expression was observed in aleurone and embryo (60%) of a plant. It was concluded that promoter PRO0175 is suitable for strong expression in calli and in seeds, more particularly in developing/maturing seeds, more particularly in the aleurone layer and in the embryo of the seeds.

PRO0177 - SEQ ID NO 22- Cdc2-1

[0102] 1 construct (OS1436) was investigated. 16 calli, 12 C, 15 B plants and 15 A plants were analysed. Expression was observed in some of the calli (31%), in the discrimination centre (42%) of C plants, in young leaves (25-58%) of C plants and occasionally in young leaves (15 %) of A plants. Moreover, very strong expression was observed in aleurone and embryo (60%) of seeds from A plants. It was concluded that this promoter is suitable for specific expression in seeds, more particularly in developing/maturing seeds.

EP 1 801 223 A2**Example 4. Stability of the expression patterns of the promoters of the present invention in further generations**

5 [0103] The above-mentioned analyses were performed on T0 plants originating from the transformed tissues. The stability of promoter activity in the next generations or progeny plants of the original T0 plant, the so-called T1 and T2 plants, was evaluated as follows. The T0 plant transformed with the reporter constructs as mentioned in the above paragraphs of Example 2, were grown until maturity (A plants), of which the seeds (T1 seeds) were harvested and sown to generate progeny T1 plants. These plants were analysed as described above in Example 3 and the A T1 plants were allowed to reach maturity and to set T2 seeds.

10 [0104] The expression pattern of the promoters of the present invention was studied in T0 plants, T1 seeds, T1 plants and T2 seeds and in all the tissues (including seeds and seed tissues) as described in Example 3. The specific expression patterns as reported from the T0 and T1 seeds and described in Example 3 were confirmed in the following T1 generation and T2 seeds. It is concluded that the expression pattern of the promoters of the present are stably inherited in plants of subsequent generations.

15 **Example 5. Stability of expression patterns of the promoters of the present invention in other plants**

[0105] The above-mentioned plant analyses were performed on rice plants. This choice was based on the practical consideration that plant genetic engineering is most profitable for crop plants. Also in other crop plants, such as for example *Zea Mays*, the reporter constructs comprising the promoters according to the present invention are introduced and transformed plant are evaluated as described hereinabove. The expression patterns of the promoters according to the present invention are conserved among plants. Therefore, the promoters according to the present invention are also suitable for driving and/or regulating expression of an operably linked nucleic acid in monocots, such as corn.

20 [0106] For many other purposes such as research and horticulture, (small) herbs are being genetically modified, which involves the use of promoters. Therefore the reporter constructs comprising the promoters according to the present invention are introduced into other plants species such as for example *Arabidopsis thaliana* and transformed plants are evaluated as described hereinabove. The expression patterns of the promoters according to the present invention are conserved among plants. Therefore, the promoters according to the present invention are also suitable for driving and/or regulating expression of an operably linked nucleic acid in other plant species such as for example dicots, such as *Arabidopsis*.

30

35

40

45

50

55

EP 1 801 223 A2

SEQUENCE LISTING

5 <110> CropDesign N.V.
 <120> Rice promoters
 <130> PF58322
 10 <150> EP 03075331.3
 <151> 2003-02-04
 <160> 88
 15 <170> PatentIn version 3.1
 <210> 1
 <211> 1264
 <212> DNA
 <213> Oryza sativa
 20 <220>
 <221> misc feature
 <223> PRO0110 - RCc3
 <400> 1
 25 tgcacgctac tcaagtgggtg ggaggccacc gcatgttcca acgaagcgcc aaagaaagcc 60
 ttgcagactc taatgctatt agtcgcctag gatattttgga atgaaaaggaa ccgcagagtt 120
 tttcagcacc aagagcttcc ggtggctagt ctgatagcca aaattaagga ggatgccaaa 180
 acatgggtct tggcgggcgc gaaacacctt gatagggtggc ttacctttta acatgttcgg 240
 gccaaaggcc ttgagacggt aaagttttct atttgcgctt ggcgatgtac aattttattc 300
 ctctattcaa tgaaattggt ggctcactgg ttcatataaa aaaaaagaat ctagcctgtt 360
 30 cgggaagaag aggattttlt tctgtgagga gagagagaga gagagagaga gagagagaga 420
 gaaggaggag gaggattttc aggtttcgca ttgcccacc tctgtttctg ttggcccag 480
 aagaatccca ggcgcccatt ggctggcagt ttaccacgga cctacctagc ctaccttagc 540
 tatctaagcg ggccgacctt gtagccacct gcctagtgtt gattaaagt gcccggccag 600
 cagggaagcca cgttgcaatg gcatcttccc ctgtctctcg cgtacgtgaa aacaaaccca 660
 35 ggtaagctta gaatcttctt gccggttgga ctgggacacc caccaatccc accatgcccc 720
 gatattcttc cggctctcgt tcatgtgatg tctctcttgg tgtgatcacg gagcaagcat 780
 tcttaaacgg caaaagaaaa tcaccaactt gctcacgag tcacgctgca ccgcgcgaag 840
 cgacgcccga taggccaaga tcgcgagata aaataacaac caatgatcat aaggaaacaa 900
 gcccgcgatg tgtcgtgtgc agcaatcttg gtcatttgcg ggatcgagtg ctccacagct 960
 40 aaccaaatat tcggccgatg atttaacaca ttatcagcgt agatgtacgt acgattttgt 1020
 aattaatcta cgagccttgc tagggcaggt gttctgccag ccaatccaga tcgccctcgt 1080
 atgcacgctc acatgatggc agggcaggt tcacatgagc tctaacggtc gattaattaa 1140
 tcccggggct cgactataaa tacctcccta atcccatgat caaaaccatc tcaagcagcc 1200
 taatcatctc cagctgatca agagctctta attagctagc tagtgattag ctgcgcttgt 1260
 gatc 1264
 45 <210> 2
 <211> 1215
 <212> DNA
 <213> Oryza sativa
 50 <220>
 <221> misc feature
 <223> PRO0005 - putative beta-amylase
 <400> 2
 55 cccgatttag tagaccacat ttggcatca aacaaaata gacctctcc cagaatttgt 60

EP 1 801 223 A2

```

    aaatggcttt gtggttcgtg atatcactga acctgctggg tgaataaagt aaaaaaaaaa 120
    acccataaat tggccttctg caagatctcg tcgtcttgcc caaactatag ccttcgatct 180
    ttccatcagg accgcatggg gggagagcag gggcaagtat gaaatggagt tcagattcag 240
    attctagaac agtctgaaca tgcgacgacg acgatggcga tgtatctgaa caatctggtc 300
5   ctctccctct cctcccgggc gggcttccac gcggctgagt ttcaggctcc caatctgcag 360
    ctctcccag aaccttactc tgattgattg gttcatcggt tccatggctc caatgaatgc 420
    aacgtgttgt tcagattttc tgaatcttgt tctcaatccg gagtacgtgc tgtagcagca 480
    gcaatctgtc cctgatctga gaattttaga cactcgtaga ttcgctgatc aatcattccg 540
    tcccttcgag tggctctagat tgagcttaat catcctgcta ctgcaatcaa atcttcagca 600
10  agtgagagct agataattca gaagaaatca acatattctt cgcgaaaaaa agaaataaac 660
    gatgaaacca cggtaattag gttcttcgaa tcaccgggag agtaggaaaa aacgagctaa 720
    aatcccacat aggaggaaac ggttaaaaac ggccactccg cgtctccgcc gcgagactag 780
    ctctcgccag tccacgtagc ccaatccaca accgccacgt gctccgacaa tcccgccgt 840
    ccatcgccgc ggccccggcc tcatctcgac cactcgtttc ctcccttcac accagccacg 900
15  tggcactctc tcgagagctc ccgcccgcct atataaactt gttcgcgctc ggctcctcct 960
    cctcatcgac ctccacccca cattgaataa ttatttttta taatttttagt tttttttttg 1020
    gcttttagata tattcccaat ccccaacctc ccaataatcc gatctctccc agttctgttc 1080
    ggatcaaggc tgtgtcgatc gcaaaaaaga aaaaaaaaac aatttccttt tggggtgggt 1140
    catctgttga tcacttcttt gtttcccgcg ttttggtggg gattcgattt tcgggttaag 1200
20  attttctaca cgacc 1215

```

```

<210> 3
<211> 1038
<212> DNA
<213> Oryza sativa

```

```

<220>
<221> misc_feature
<223> PRO0009 - putative cellulose synthase

```

```

30  <400> 3
    gccatcgagt ggtgtgccga taccggcgcc tgttctttac agcctcagct agtgttggtg 60
    tccgaggcaa tttttccgac ctattgtgtt gctttcctct ctgatagctt atggtaaaag 120
    atacaaagat gttgaggagt ttgtacgcca cttaattttg ctgtaacat acattgacaa 180
    tcaagaggag ccatggcatt gcgatctgct tacacggcat attcttactg gatggtgtac 240
35  actacttacc ctttttaatg caagcatcaa tccattgctt ttctcactgc acacctgatt 300
    cgtactgaaa acgtgaaaca taaaaaaaaa acaaaaatct agctgatgtt ggctctcggg 360
    gcctcgagtc tagtttgtcc tagatggcta acctgatatg tgttggtcac gctcacgttt 420
    gaaccgagaa agagtgtgtg tgtgtgtgtg tcggcgtgct gctacaccag agcctccctg 480
    aatcgcaatg cgtgttaacg ccagcatcgc aggatttcat ctcaactgac aggttcagat 540
    ggcttctctc ctaccgtctg ccattttatac acgcagtgac ttaacgctta cacgagccgg 600
40  atggcccgga tctccccctt gcaccatctc accagaaaaa cggtgaggcg tcaccgcaac 660
    ccaccacca aacacatcca cgtcccttca ccgttggcct tcgattttgc ttcagctgca 720
    ctacgacccc tccaacacat ttccctcgcg tctcgttgcg atctcacctt acgacgatct 780
    cgttccagca gcagcagcat cggcagcggc ggcttgcttc cgaagcgagc aatgcatggc 840
    gcgcgcggcc gcgtgcgtgc gtgccttggc ttgcgctcta atcaaaccgg gacgccccaa 900
45  ctacgggttg gtgcgggacg ccaccccgcc accttaccgc cccgcctcc ctgcacttga 960
    tcatcaacca gctgctatat cacctagcta gccgcgcct cctcctcgcc caccaacgctc 1020
    gtttcccgcg cacctcac 1038

```

```

<210> 4
<211> 1301
<212> DNA
<213> Oryza sativa

```

```

<220>
<221> misc_feature
<223> PRO0058 - proteinase inhibitor Rgpi9

```

EP 1 801 223 A2

<400> 4

	tctcttctga	agctgaagcc	ctgcgaaata	ggcctttaaa	cgctttaagg	ttactggatg	60
	atcatatcgg	cgtaagaccg	gtttaaacat	ggtttcgctt	tgtgaatcca	atgtgagtca	120
	cgacgtgaca	catggcacgt	ccttggagct	ttagacatat	cgaatctgag	cactggagtg	180
5	gccgagtggg	tgagcggcca	aatcgcgttt	agacagatcg	cactgacacg	atgttgatca	240
	ttgatactaa	taccatttta	tcaagcagta	gtgttgaaaa	aaaaacttat	gttctcttca	300
	actgtgagat	ttcatcccgt	ttcaagatga	acaagccatg	catgtgagat	gtgaacagaa	360
	ggcagaagac	agtygaazga	caygacaaat	aagtgaagag	ggatcaaata	aatgggcctg	420
	acggtttctg	aaagttgaca	tggaatcgc	cggatgacac	cggttttatac	gttattttaaa	480
10	tctgcgattt	ccactttcgt	ttgctttcgg	ggttccaatt	tgagtcacgc	acataattctt	540
	catcgtgctt	tggtatctcag	caccgtagta	acttttggac	aaattgcatt	cgccgacact	600
	aataecatgt	tctttttatg	ctgctttaca	tatactgctt	atccacaccc	aatcccattgt	660
	tcatatatta	tgagatggag	ggagtaaact	ttgttaacag	caacattttt	tatattaaag	720
	catcaactaa	ttaaagcaca	agatacgcct	gttatctcaa	taaatcttcc	agtgcattga	780
15	taaagaagat	gtcgcgcgta	acttagataa	tttttgtgac	ttttatcctg	gccggcataa	840
	ttaattcttc	cggaaattaa	aagctagtgt	ttccatattc	atcagtacag	acaagacagc	900
	atagtaagcg	aagcatacct	gacgtgttag	ctcattgtaa	ctcgtatctg	aacactcgat	960
	gctagatata	gacagacact	cctcgtgatg	aacgttagca	tttagcaaca	tacggtgata	1020
	aagcagctgg	ggatcgatcc	atccatccat	cgtctttaca	cgtacttacc	ttgctaaccg	1080
	cactgtcgac	tcttgcattg	ttgcatgtaa	tccaaatgga	ccccacgtgg	aacatgctca	1140
20	cagtgccttg	cagctgcttt	ccaaaatgct	ttctttcact	tcttccattc	ctctgtccac	1200
	aaaaaaagta	gtgtgttctt	gagcctatat	aagagagggt	cacacgctcc	agtcgactca	1260
	ccatcgatcc	atctgacggt	tagttccaag	ggaaaagaaga	a		1301

<210> 5

<211> 1243

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<223> PRO0061 - beta-expansin EXPB9

<400> 5

	aaaaccaccg	agggacctga	tctgcaccgg	ttttgatagt	tgagggaccc	gttgtgtctg	60
	gttttccgat	cgagggacga	aaatcggatt	cgggtgtaaag	ttaagggacc	tcagatgaac	120
35	ttattccgga	gcatgattgg	gaaggaggga	cataaggccc	atgtcgcgatg	tgtttgagacg	180
	gtccagatct	ccagatcact	cagcaggatc	ggccgcgttc	gcgtagcacc	cgcggtttga	240
	ttcggcttcc	cgaaggcgg	cggccgggtg	ccgtgcgcgc	gtagcttccg	ccggaagcga	300
	gcacgccgcc	ccgcgcgacc	cggctctgcg	tttgaccgcg	cttgcaacgcg	atacatcggg	360
	atagatagct	actactctct	ccgtttcaca	atgtaaatca	ttctactatt	ttccacattc	420
40	atattgatgt	taatgaatat	agacatatat	atctatttag	attcattaac	atcaatatga	480
	atgtaggaaa	tgctagaatg	acttacattg	tgaattgtga	aatggacgaa	gtacctacga	540
	tggtatggatg	caggatcatg	aaagaattaa	tgcaagatcg	tatctgcgcg	atgcaaaatc	600
	ttactaattg	cgtgcatat	atgcatgaca	gcctgcatgc	gggcgtgtaa	gcgtgttcat	660
	ccattaggaa	gtaaccttgt	cattacttat	accagtacta	catactatat	agtattgatt	720
45	tcattagcaa	atctacaaaa	ctggaaagca	ataagggaata	cgggactgga	aaagactcaa	780
	cattaatcac	caaatatttc	gccttctcca	gcagaatata	tatctctcca	tcttgatcac	840
	tgtacacact	gacagtgtac	gcataaacgc	agcagccagc	ttactgtctg	tctcaccgtc	900
	gcacactggc	cttccatctc	aggctagctt	tctcagccac	ccatcgtaca	tgtcaactcg	960
	gcgcgcgcac	aggcacaat	tacgtacaaa	acgcatagac	aaatcaaaac	caccggagaa	1020
	gaatcgctcc	cgcgcgcggc	ggcggcgcg	acgtacgaat	gcacgcacgc	acgcccaccc	1080
50	ccacgacacg	atcgcgcgcg	acgcgcgcga	caccggccat	ccaccgcgcg	cctcacctcg	1140
	ccgactataa	atacgtaggc	atctgcttga	tcttgtcatc	catctcacca	ccaaaaaaaa	1200
	aggaaaaaaa	aacaaaacac	accaagccaa	ataaaagcga	caa		1243

<210> 6

<211> 1019

<212> DNA

EP 1 801 223 A2

```

<213> Oryza sativa

<220>
5 <221> misc_feature
  <223> PRO0063 - structural protein

<400> 6
10 cctagctata tgcagagggt gacagggtgt ctcttagatc gattaataat atcacattga 60
   tgcaattaat tatctgagat caataaagtt tttctttatg ttaaattaat atcagtaata 120
   gatgctaagt ccttcattag tagtatccca catttaatca cagttggaca cacaaaaaaa 180
   aaggcaatgc cattaatatg ccatctctct tgttttccat tgcctaccac gtgccatatg 240
   atatcatcat caggcacacc aatccataac tagttcatta gagcaagttt aataatagag 300
   ctaactataa gcttataatt tatattggag taaacatgta tagtaaatga gctataaggt 360
   tatttctttt tttctcctcc tctctctatc tcttacctat atatttaatg tatttgtctt 420
15 gaagtatgtg aatagctagc tcttgtagta gagccaatcc tctgcatttt ttaaattctc 480
   tttctctcac ataagcatat agttggctta tagcctgcta ttatacttgg tcttagtaca 540
   ctaaccccc ttacatgcaa tgcaagctgt ctaattaaaa gggtttcaca acattttgaa 600
   tgccactact agctcccaac caccaaccaca gatctagcta gggtttgctt atttctctcc 660
   tctctctccc tctctcttcc cgttgtgcca attcatccaa agtcattgag agccatacta 720
20 ctcacatatca tattactcct acatgtgtac tacatttata ttgatgatct gtaagagcaa 780
   aagtattaat ggggatcaca ggattgcagt aacagcagca ggtacccctt cctttaacat 840
   ccgcagttac gctcccccac taccgtcttc tctgcgagc gatgacgatg agcttctcct 900
   ccgctataaa tctctctccc tctctctccc ctcctctccc aactccacat cgatcagcag 960
   cagcagcagc ttgcacactc gagcttagct tagcttttgc aagagagatc gagctagag 1019

25 <210> 7
   <211> 1212
   <212> DNA
   <213> Oryza sativa

30 <220>
   <221> misc_feature
   <223> PRO0081 - putative caffeoyl-CoA 3-O-methyltransferase

<400> 7
35 atggtgcoat gtcaataaga catcataata gaaactacac tccacaaccc atagtttctt 60
   aaagtgggtc attaataaat acatcatcta tctttctat caatcatatt tattctttat 120
   ctattatgac ggcactatct tctcccaatg taaaacttga taatgtctag tgcatagggt 180
   ctctgttgga agctgtttct tacatgagac ccagtttctt cttctctcca ctctctctta 240
   attaatataa tgtcacataa gttaaaagtt ctagtaataa ataatatagt taatgacata 300
   gacaacatcc tagatgtagy gttaggagtc ttcgagacgt agcaaccctg ttttgactcc 360
40 ttttttggtc gcccattcac agtcgccacc agaaaattca ctgtgcccaa atcaatggaa 420
   ggcctacta gatccatcca tcttcgtgac agctccgagc tttctctctg ttatttttct 480
   cccaaaaata cattcagaac acgatctcaa atttaaaacta atggagtgtc actgcatttc 540
   ttaattataa gtgcgagcac cactcattaa tcatttccat cacaggtaaa tctgtgtgag 600
   ctggtggttg ctactgtact actagtacta cctgtcgcag ctttgtagaa gccgttttcg 660
45 ctgaagcttc ttcttcttcc ctgggcaaaa taattttaag caggcggaat aatattggga 720
   taaacagggg ggacaaaagc gtgcgatccc tttctttaac caaaccacga cgaaagcagg 780
   ttaggtcgcg gcaggtggtg gtggtaggaa gaagaagaaa gagaggggaa aaaaaacaaa 840
   aatttcacat gcatcatgca tgaagtagta catgtagtac tgagtactgt aataatgttc 900
   agtttactgg accgtctcaa cgggaagacc aaattaacgc ttataaaata cccttttttt 960
50 gggcactgat catggccact acgttttggt gctcaacaac caggtcaccg tgcgatcgat 1020
   cgattgtctaa tttatttttt gaaaaggaaag ggaggaaaaa agaccgggtg tttggtggcg 1080
   ccaccaaccc tgcctctctg agccgataaa tattgtctgc cggagctctc ggttgacgac 1140
   ccaaccaatc gactcgcacc accaccagca gctcaagcag caacagctca aacggaggaa 1200
   gatctcatcg cc 1212

55 <210> 8
   <211> 1052

```


EP 1 801 223 A2

<212> DNA
 <213> Oryza sativa

<220>
 5 <221> misc_feature
 <223> PR00091 - prolamine RP5

<400> 8
 10 gtttttctat gaaccggtca ttaaaccgtc cccggttaga ccgaacaagc cacaataatc 60
 ttgaaatggg ccttgatgtg gcccaattgg tctgcctaga gcgttttggg tggcaaaaat 120
 caatctccta ttctcggcac gtgtgatata caatggtaag tgagatatac aattctcggc 180
 acgggtacat tacaagggtg cgcattgtgt caatgtttgg ttaatttgct agattcacat 240
 aatacatgcc aggaagtcca gaacaatgtg ttgcctttca ccggaaaact ttgttgagc 300
 aaatgccttc ttcttttttg cttctgcttc ttgagtcctat gtggaggaag cagtagatag 360
 15 ctgatgatat caggattcct tctgtgtctg tgtaggtgta gcaacaccac tataattttt 420
 atttagcaac acaatatcaa tttggtctat aaaagtatga attaaatcaa tccccaacca 480
 caattagagt aagttggtga gttattgtaa agctctgcaa agttaattta aaagttattg 540
 cattaactta ttctgtatca caaacaagtt ttcacaagag tattaatgga acaatgaaaa 600
 ccattgaaca tactataatt ttttttctta ctgaaattat ataattcaaa gagcataaac 660
 20 ccacacagtc gtaaagtccc acgtgtagt cattatcaaa ataatagctt acaaacata 720
 acaaacttag tttcaaaagt tgcaatcctt atcacattga cacataaagt gagcgtatgag 780
 tcatgtcatt atttttttgc tcaccatcat gtatatatga tgggcataaa agttactttg 840
 atgatgatat caaagaacat ttttaggtgc acctaacaga atatccaaat aatatgactc 900
 acttagatcc taatatagca tcaagcaaaa ctaacactct aaagcaaccg atagggaaac 960
 atctataaat agacaagcat aatgaaaacc ctctcatcc ttcacacaat tcaaacatta 1020
 25 tagttgaagc atagtagtag aatcctacaa aa 1052

<210> 9
 <211> 1216
 <212> DNA
 30 <213> Oryza sativa

<220>
 <221> misc_feature
 <223> PR00095 - putative methionine aminopeptidase

<400> 9
 35 cctgatggat gatgaatcac tgatcgattt ctagttctta ttctctgaag atgaaccgaa 60
 gatccaagat tgytccatga aattatcctt tcttgatttg gccctccgag aatagattcc 120
 tgtgcaatct agtcagtagt tggtcaggtc atgtaaacgt acggtaagaa atttatgtgc 180
 agagggtttt ccagtttatc ctatgcattt gacctctggt catgtattga ttctgagaca 240
 40 aagtgtagt atcgcttgat gatactagta cacattgctg ccttcttttt tgcctgtaa 300
 aagatttatt attggcagca atggatggta gagagggcaa tctgcttctt agttttgagt 360
 ataaagtttt aagttttgag cagagtttcg aaaatttgca gtagaaagt tgaattttca 420
 aattggaagt acagtttttc aaatttccag tataaatttt taaaccact gagaaaccaa 480
 gagcatatgg gcgatcaaaa atttcttttc taaaggaaaa atatttttta aaaaacactt 540
 45 agtagtatat caaaattctg aggtaaagctc attaggccca ttcactgtac ggcccatgaa 600
 gcccatgtct gtgagatggg cctaccctgt caggcagaga tggatgggccc ttaatttgta 660
 ggcccatgtt ggaagccca ccaaagccca ataatatatc ctctcacct tcaaccctaa 720
 tcctcctctt cttctagaag actgaaaatt cctctccttt cttctctcgc cctcaccgct 780
 cgccgaggtt gccgtctcct tgtctcctcc gctccttgcg ccgccgcgcg gacgagtcgc 840
 50 ggggaggggg ggcgatctcc atctccatct gaggcgagga gagcagggga ggtgagggga 900
 tcctggtgag gtgagcatcc acgtcctctt tcttttttct tgattcatct ctctctctct 960
 cgcacatcgg gactggaatt tgcctgctgt cgttcgttaa gtttaacccta gcttctcttc 1020
 tagatctgga agaaactctt cttcttttaa tttcagagcc ttaaccttaa tagtacaagt 1080
 aacagtttgt ttgttccccg aaaagtttgg atgcctcca aatagagaca catgttattt 1140
 attttggaat gtaatttgtc cctggattta ttcattcagg tttgtgatta ctggacaata 1200
 55 gaaatattta cacaat 1216

EP 1 801 223 A2

```

<210> 10
<211> 1237
<212> DNA
<213> Oryza sativa

5
<220>
<221> misc_feature
<223> PRO0111 - uclacyanin 3-like protein

10
<400> 10
tcgttaagtt tgatgatttc tgatgaccca tggtcaccta gcggctagca gtaccatgca 60
tgatcacccct ccacaaagaa atggtacagt acatctccgt cccaaaataa gtgcagccat 120
gtatatccat gcctaacggt tgaccgtccg tcttatTTaa aaaaattatg aaaaatttaa 180
aaatatttag tcacacataa agtattattc atgttttatc atctaatagc aacaaaaaat 240
15 actaatcata aaatTTTTTT taataagata aacgggtaaa cgttgaacgt gaatagtgc 300
aaacttattt tagaacggag ggagtacgaa gtaactccgg aactacatat agggcaatta 360
ttgccctatg tatgcatata gtcaatcaat taactgctga caatggaaaa gctaatacat 420
caatcaatgg tttgattaat caaattaagc caggtcagtc cgtcagtgtg cattcactaa 480
ttaaattaac aggtttgttc aacggttcaa ccaacatctg ccatcaacat cttttcgttg 540
cacctttctt gactctttat gctattttgc taaaaaaaaa cttctcttta catcacttat 600
20 aacaatatat atttctgctt taatttgtaa tctttttttt ctgcgttgca acggaaatca 660
cgagcgatat atggtgaaga ctgatgataa tcgtatttct gatgaccat gattccgcgg 720
tgtaccatct gttctgtcaa ctaaaaagtg gagttagttcc ttgacggaag aaggagcaa 780
aatagaagat attctcagtt gatctgcagt tgtgttagg tcaatatatt cagaaatcgc 840
agttgctggt gtttaaattg tgtgtgacag cagacagcta attatcagta cacgtatatg 900
25 agcaatacta gtgaatctgt actaatttaa cgagagtatt ttctatatac aaatacaaca 960
gcaaaactgt gccactggcg ccgaatacgt acggacagag ctcaggcaat caggggagca 1020
gcaaaagagg agagagttgg tgccaagcac aactaaaccc aactgcaccc aaaaactaat 1080
cagcatttca gttcgcttta gttagtacta ccacctgcat ctctttacca acactatata 1140
accgcagtg gacctgcagt catctcacta attcagtga gccaccagta ctagtacggc 1200
30 tctaatacgt tcgcgtttgc taattaactc tgccatc 1237

<210> 11
<211> 1100
<212> DNA
<213> Oryza sativa

35
<220>
<221> misc_feature
<223> PRO0116 - 26S proteasome regulatory particle non-ATPase subunit 11

40
<400> 11
ctaagggcag cagccattgg gctctatagg tgtggttgca agtgcaacta caagcgagca 60
acctggtaga atatccccga gatcagtagt taccgtgatt ggttcagact tgagaggcta 120
atTTTTtctg acctgtagct ttattacatc gcatttcctc ttattgaagt ttagccgagg 180
tggtgcggat ggatattcag tctaacagac tcaatgaacg ctttggtgta tgacttgtag 240
45 agtactggct gctcgaacag gatggttcag cttccagaaa tttggcaacg ctccatttca 300
aagaaaatca ttcagtattt gccttctgtg tgttacattg atctcatata aagtcacttt 360
gatcggtgac atcttgTTTT ttggttcggt tgccatggta gtttcccttg ctgctgggag 420
gattgccgcc tgaactTTTT cttttttgcg aggatgttat ttttgccaga caagaacggg 480
aataagcaaa ttggttggtg gaactaaagt aaactcgatc tctttccgag aagtgtatta 540
ttttcacgtg taccatcaat ttttttgaaa gtaaatattt ttccccttta actaatgttc 600
50 actttggacc ggataatctt acctttattt aactttgggc tatctaactc tcttctaaag 660
catataaacg atcttgagta catcgattcc tacttatcat ttaactctcg tagcttaatg 720
taagattatt tctttgaaat atgataaatt ggatgcatat gaatgaaaga gtcaaggatt 780
aagtgattcc tcaaaaaaaa aaaagagtga aatttattta tttttccctt ttcgacacga 840
agaagggctt ggttgaggga aaatggccca gatcagatg accgaggcgg agtaccatgg 900
55 gcccacaaag aataataagc cccgagccca aacgctaagg cccacgagaa gccgtgcgct 960
ggaagaaaga aagaaaccgc ggccgtcttc acaccgaagc ggcgagcag acgactcgca 1020

```

EP 1 801 223 A2

```

gtcgcagcct ctttcctcct ccgtctctct ctccccctct cctctcctcc gcgcggcgaa 1080
cgaagcgagc gagcgggcgc 1100

<210> 12
5 <211> 1216
  <212> DNA
  <213> Oryza sativa

<220>
10 <221> misc_feature
  <223> PRO0117 - putative 40S ribosomal protein

<400> 12
15 cgtgttcatg ttgcatttta ggattggact tttttaggat ggagaggata tgtcctaacg 60
   gaaatgtcat gtctatgctc cgatcttata aatttgttca atagcgttgc aaacgcgatc 120
   attaaaaagg cggtaaagaga actaccacat tttcgaaagc ccattctctt cgtgagttac 180
   tggaattatt tggcatagca catgcataaa gatgctttag taatgagctc aataaaacac 240
   gacagctttg catgtagcca caatgctata gtaaagagt tgtacttctt ttgcattgca 300
   aagtgttact gaccttgttt aggcagctag cttcattcat tttttgaatt ctatagttat 360
   agttataaag attatcataa tttagataag aatccggtat gtttgagaag ctggagtttc 420
20 tagagaagct ataacaactc gaagctccct aaacagagcc attgaacatt gagctgtcca 480
   gtatatcatg acaaaatgat acattttgca tgggcatatg tgtctaagaa aacaaacatc 540
   acaattcaat gagtcactct aaaaaaaaag gcaaaacact caacaaaacc ataccgtgaa 600
   agtgaaccta taatgaaatg aaattttgat aagcatgctt acccaggtgg aaatttcaat 660
   ctaagaacaa tttccaaaac caccgtccat agaaatatgt ggaattcatt cagaattttc 720
25 ataccacacg ataaaattta tagggaattt aacttttgcc atttttaccg aacaccacct 780
   tttcatttgc tcctataatg ttatcgaaaa gagagtgttt gttaattatt tgtcactttt 840
   atcacgacat gtacgcgtga caacgtggcg ttctctgttg agcccacccg tcagccgccg 900
   tacgcaccac catcaaagaa ttcaagacgg agagcgtcgt cgccgtcggc aaggcggcgt 960
   gttttgttca ctgtacgttg cttcggcgtg ggcccaatct tgttcgggac taactagttc 1020
30 ttcccagccc aggccatta agcctaccaa cccggacggc ccgggaggag ctagggtttc 1080
   acccttcaat atataaacct ctctctcctc ctccggccgc cgcctccgaa gccctagctc 1140
   ctcccgccgc cgccgcgccg gccgcgccgc cctctccact cgagagaccc agccgcgccg 1200
   gccgcgccgc ccgcca 1216

<210> 13
35 <211> 1210
  <212> DNA
  <213> Oryza sativa

<220>
40 <221> misc_feature
  <223> PRO0122 - chlorophyll a/b-binding protein presursor (Cab27)

<400> 13
45 cagatgccac agtatggtgt accaccagct gctccacacc atgctccacc ggctggccaa 60
   ccaatgtatt tcccgaata atctatcttt atccgatgta caagcaatta gagcaattgc 120
   aaatgttgcc tgcaatactc gggctctggg atcttctctt caaattttgg gttgtaactc 180
   gtctatgcag ctattcatat tgtaactcag tgagctccct gtcgcaaatg tgcctctgcg 240
   tcagtgcgtg tctgtaaact gtccggcaat tagaaattcc catccttagc atgcctggta 300
   ttgttcagct cgaactgaa atttttcttc gtgccctata ttttttcggg ttagataagt 360
50 gttccgctgg aattttatgc aggtgctgta cccatgtgc tgcctttttt ttgtgtgggg 420
   cgcccccccg gggggggggg ggggtttcct ggcatgattg caaataagaa ccccggggca 480
   aatctgctgg ttggttgcaa ataataaccc ctccaaatct gcgcagatga aaccccatc 540
   aggacatgaa ttacgattgt tcatgagcta tttggatcat ggaaagattg gaaacaaaca 600
   cttacgtcaa ggtttctact aattacgtga ttccgatttc agagtcagcc atggctatac 660
   tgcctttgct ccagtaaaca tcgctgctct agtaacaaac attgcagtaa acatcacaaac 720
55 tatccaattc cctgttgct gctctagtaa aaaacattgc aattatccaa ttcccagata 780
   ttttctttca ctactccaaa acctaaagta catatactg agttgagtga tccagcaaca 840

```

EP 1 801 223 A2

```

5      taaaaatccg aggctccgag cgatctgcac caaccatctc acccgctccga cgtggcagca      900
      gcaaccagcc acagctgaga cctccatcca atagaaaccc tccctttgat tccccgtat      960
      cccggcatcc ggataacgct ggataagagg cgacgcctcc cattggccac acccacccaa      1020
      caacgcaccc tggcgcgtcc atccaccccc accgcccgatc tccgcccgtcc gtcgcccgcc      1080
      tcgccaccgt ggccacctgg cagcgccggc cactcccga cagtttaata caagccacgc      1140
      ctttgctccg tgcgggcca aacgtaccct tgtgactaca cccgcttcgc ttcctccct      1200
      ctctaagccg                                     1210

<210> 14
10    <211> 1179
      <212> DNA
      <213> Oryza sativa

      <220>
15    <221> misc feature
      <223> PRO0123 - putative protochlorophyllide reductase

      <400> 14
      ttgcagttgt gaccaagtaa gctgagcatg cccttaactt cacctagaaa aaagtatact      60
      tggccttaact gctagtaaga catttcagaa ctgagactgg tgtacgcatt tcatgcaagc      120
20    cattaccact ttacctgaca ttttgacag agattagaaa tagtttcgta ctacctgcaa      180
      gttgcaactt gaaaagtga atttgttct tgctaataata ttggcgtgta attcttttat      240
      gcgttagcgt aaaaagtga aatttggtc aagttactgg tcagattaac cagtaactgg      300
      ttaaagtga aagatggtct ttagtaaatg gagggagtag tacactatcc tcagctgatt      360
      taaatcttat tccgtcgtg gtgatttct caatctcca acttagtttt tcaatatatt      420
25    cataggatag agtgtgcata tgtgtgttta tagggatgag tctacgcgcc ttatgaacac      480
      ctacttttgt actgtatttg tcaatgaaaa gaaaatctta ccaatgctgc gatgctgaca      540
      ccaagaagag gcgatgaaaa gtgcaacgga tatcgtgcca cgtcggttgc caagtcagca      600
      cagacccaat gggcctttcc tacgtgtctc ggccacagcc agtcgtttac cgcacgttca      660
      catgggcacg aactcgcgtc atcttcccac gaaaacgac agatctgccc tatctggtcc      720
30    caccatcag tggccacac ctccatgct gcattatttg cgactcccat cccgtctcc      780
      acgccc aaac accgcacag ggtcgcgata gccacgaccc aatcacacaa cgccacgtca      840
      ccatatgtta cgggcagcca tgcgcagaag atcccgcgac gtcgctgtcc cccgtgtcgg      900
      ttacgaaaaa atatccacc acgtgtcgtc ttcacaggac aatatctcga aggaaaaaaa      960
      tcgtagcgga aatatccagg caccgagctgc gattggctgg gaggcgtcca gcgtggtggg      1020
      gggccacccc ctttatctt agcccgtggc gtcctcgtc cctcgggtcc gtgtataaat      1080
35    accctccgga actcactctt gctggtcacc aacacgaagc aaaaggacac cagaaacata      1140
      gtacacttga gtcactcca aactcaaaaca ctcacacca                                     1179

<210> 15
40    <211> 1808
      <212> DNA
      <213> Oryza sativa

      <220>
45    <221> misc feature
      <223> PRO0133 - chitinase Cht-3

      <400> 15
      ttggcgcgg ggcagaagag tggactttaa ctttcttttt aataaaatct ccaattaata      60
      tgtaattata atatacttt aatcaaaaca tgcaaagcta gcagtattta catcactaga      120
      agtaaatctt tcttgctcat gatgcttcag ccggacggaa ccctaaaata tagatggggc      180
50    ggatacactc gattaaaaca gctaattgca acacatatca tataaggttt tggaaattcat      240
      accaaatgct ccgaaattcg tctatttoga tgaggcccaa gacatgacct cctgtttcgc      300
      ccatagttta tgggtgttgg taaaatttgg ttaaaatctg tctattttag taggtccoga      360
      aattcttatg caattgaatc ctagaaccct atcatattta tattgcaatt gcacaaaaat      420
      aatgtgcaat caatatattc caattgcaat acatatcaag catgaggtgt aatacatatc      480
55    cagccgctag cactgggtct gttgaggtgc ttcttgagc aacagctgca atctgtttgg      540
      ctaggctgtt ggcgcaggc actgctgtcg tgctgcaaca atggcacatt cgtcgagcac      600

```

EP 1 801 223 A2

5 acaaccgagc ctatgcacag cgcaagctcg ctgccttggg ccgtgggtcc agtggtgcat 660
 caaggcttag tggattgagc gagaagacga actgacaatg ccaaagatgc gatgctgcga 720
 gtgtggactg cggaagatga atcgagatca atcaattcgt tatgcttgaa aggctggaat 780
 aactgatcag ttggttgat cgatggatg tactagataa tatgcggtct aggcctagac 840
 caagaagcag aagaggagtc gggtcgggag tgtggggcga cgtaggctgt agctgggccc 900
 gccgccccag gccgcctaact gagtgtgtcc gccctggcc tgacacgatg ggtaattaaa 960
 tagttatgca tgtccctctt tgtctaaaca atatgtataa aattgacgat atcttgggca 1020
 aaatcactgg gcatggcaca caggagagct actttagcga catgaatcta ggcgaaaatc 1080
 tattgaacca aaaatcgact gtaatctcat gaaaattttc gtcataatta tagcaaaatc 1140
 10 gttgttggat tgattgcacg agaaaacaga agaagggagc taggtgatat tatattgttt 1200
 tgttgccctac ataaatctta aagcaatcga atggtctaaa atttacaaga tttttaaaga 1260
 gggttttcgta ccgtatagac ccggccggg tcaaaacttat ttggtcgtcg ctgggtgttt 1320
 gtagcacgcc agctccatat atgtggattg cagctgggtct atgataagtt cggtcgatct 1380
 gagatcaatc tatcaatcgt caaccctttg cctttgttag cgagctagcg tgtacacatt 1440
 15 tcaattatat atgggtgcatg catggcatcc acgcctccac ggtcaacgtg gaaatatctc 1500
 tggaaactta ctttttctaa ataactgaac ggattggagg caggagacaa atttgaccaa 1560
 cacaatatat ccacgacggc tagacaatac tagtagatgc atgcatggaa ggatatagta 1620
 gtacttgtaa atcgtggaaa ctttggtaat gcgaatgcat ttcaattcgt tgctgaagat 1680
 cgatgcacca tgcatatcca tctctatata aagccatgcg atccccacca ttcttgca 1740
 20 cactactagct acttctactt ctatcatacc aaacaaacta gcttaatttg cattgcatca 1800
 cattgccg 1808

 <210> 16
 <211> 1828
 <212> DNA
 25 <213> Oryza sativa

 <220>
 <221> misc_feature
 <223> PRO0151 WSI18

 30 <400> 16
 gcttgagtca tagggagaaa acaaatcgat catatttgac tcttttcct ccatctctct 60
 taccggcaaa aaaagtagta ctggtttata tgtaaagtaa gattctttta ttatgtgaga 120
 tccggcttaa tgcttttctt ttgtcacata tactgcattg caacaattgc catatattca 180
 35 cttctgcat cccattatat agcaactcaa gaatggattg atatatcccc tattactaat 240
 ctagacatgt taaggctgag ttgggcagtc catcttccca acccaccacc ttcgtttttc 300
 gcgcacatac ttttcaaact actaaatggt gtgtttttta aaaatatatt caatacaaaa 360
 gttgctttta aaaattatat tgatccattt ttttaaaaaa aatagctaat acttaattaa 420
 tcacgtgta aaagaccgct ccgttttgcg tgcaggaggg ataggttcac atcctgcatt 480
 accgaacaca gctaaatct ttgtgtctag attcgtagta ctggatatat taaatcatgt 540
 40 tctaagttac tatatactga gatgaataga ataagtaaaa ttagaccac ctttaagtctt 600
 gatgaagtta ctactagctg cgtttgggag gacttcccaa aaaaaaaagt attagccatt 660
 agcacgtgat taattaagta ctagttaa aaacttaaaa aataaattaa tatgattctc 720
 ttaagtaact ctctataga aaacttttac aaaattacac cgtttaatag tttggaaaat 780
 atgtcagtaa aaaataagag agtagaagtt atgaaagta gaaaaagaat tgttttagta 840
 45 gtatacagtt ataaactatt cctctgttc taaaacataa gggattatgg atggattcga 900
 catgtaccag taccatgaat cgaatccaga caagtttttt atgcatattt attctactat 960
 aatataatcac atctgctcta aatatcttat atttcgaggt ggagactgtc gctatgtttt 1020
 tctgcccggt gctaagcaca cgccaccccc gatgcgggga cgctctggc cttcttgcca 1080
 cgataattga atggaacttc cacattcaga ttcataggt gaccgtcgac tccaagtgtc 1140
 50 ttgcacaaa caactcggc ctcgggcca ccagtcacac gactcacggc actaccacc 1200
 ctgactccct gaggcggacc tgccactgtt ctgcatcgca agctatctaa aattctgaag 1260
 caaagaaagc acagcacatg ctccgggaca cgccgaccc ggcgaaaag ggctcgggtg 1320
 ggcgatctca cagccgcata tcgcatttca caagccgcc atctccaccg gcttcacgag 1380
 gctcatcgcg gcacgaccgc gcacggaacg cagcgggccg acccgcgcg ctcgatgcgc 1440
 gagcccatcc gcccggtcct ccctttgcct ttgcccgtat cctctcggtc gtatcccggt 1500
 55 tctctgtctt ttgctccccg gcgcgcgcca gttcggagta ccagcgaaac ccggacacct 1560
 ggtacacctc cgcgggccac aacgcgtgtc cccctacgt ggccgcgag cacatgccca 1620

EP 1 801 223 A2

```

5      tgcgcgacac gtgcacctcc tcattccaaac tctcaagtct caacggtcct ataaatgcac 1680
      ggatagcctc aagctgctcg tcacaaggca agaggcaaga ggcaagagca tccgtattaa 1740
      ccagcctttt gagacttgag agtgtgtgtg actcgatcca gcgtagtttc agttcgtgtg 1800
      ttggtgagtg attccagcca agtttgcg 1828

      <210> 17
      <211> 1267
      <212> DNA
      <213> Oryza sativa

10     <220>
      <221> misc feature
      <223> PRO0169 - aquaporine

15     <400> 17
      cgtcctcctt ttgtaacggc tcgcaaatac aatgggttgt ttagattcat gtcatttttaa 60
      atcatattat tttttataaa gttatcaaaa tgtacatata tttatttatt tttaccaaac 120
      ttactaaat gagataatcc aacaaatggc atttaaagcg ttcaaatcca agaaatgcca 180
      tcgccgttat gttcccgctc gtttcacgcc gttaaataac aatgttcac cttataacact 240
      taatgggtgtg gaatggacgg aaccctaacg gcgatggcat ttttgggata aagtcgtttg 300
20     tacgatggca tttcttagaa ctcatatttg tcgatggcat tttttgaatt tggatgattg 360
      tcaatgggat tttttggatt atctcttagt aaatacataa ggaatcatgc caaaacttga 420
      caatattgtc aacttatcaa aatttaattg ggattatttt ggcgataata tgaacagccc 480
      ttacatttct gaagaattat agtcaataa tggctatggc cctgtttgga ttcggagggc 540
      tatttaatag ccctccgga tcttgctatt taagagtatt aaacgtagat tactgataaa 600
25     actcattcca taaccctac gctattctac gagacgaatc taacgaggtt tattaatcca 660
      tgatttgcta cagtaatcag ccgctaactg tggattaata tacatcatta gattcgtctc 720
      gtaaaatagg ctagggatta tggaatcggg tttatcggta atctatgttt aatacttcta 780
      aatagcaaga ttccgaaggc ctatttaata gctcggagca tccaaacaag gcctatgttt 840
      agatccaaac ttccaacttt ttctatcaca ttaaactgtc atacatacat aacttttcag 900
30     tcacatcgta ccaatttcaa cccaaacttt caactttgga agaactaac acagcatatg 960
      acagtgcagt tcagctcaat tttgttcgga gcctaaaaaa aagaaaagaa aaaaagctca 1020
      atttgataa ggctatgaat aaactcaaaa aagcatccaa cctaaccacc acactggccc 1080
      accagggcc acgtccact cccgtgatca tcacctcctt cctttccag aaccaccttc 1140
      tcttccttc ctctcttct tcttcaagtgt actctgcctt tataacaccc tactctctc 1200
      tctcacctcc accatctagc tactcacac agtctccact cacacgcatt gcagaggaga 1260
35     gccgaca 1267

      <210> 18
      <211> 1130
      <212> DNA
40     <213> Oryza sativa

      <220>
      <221> misc feature
      <223> PRO0170 - High mobility group protein

45     <400> 18
      catgaggcta atgtagatgc tactgcgct agtagtaagg tactccagta cattatggaa 60
      tatacaaagc tgtaatactc gtatcagcaa gagagaggca cacaagttgt agcagtagca 120
      caggattaga aaaacgggac gacaaatagt aatggaaaaa caaaaaaaa caaggaaaca 180
      catggcaata taaatggaga aatcacaaga ggaacagaat ccgggcaata cgctgcgaaa 240
50     gtactcgtac gtaaaaaaaa gaggcgcatt catgtgtgga cagcgtgcag cagaagcagg 300
      gatttgaaac cactcaaact caccactgca aaccttcaaa cgaggccatg gtttgaagca 360
      tagaaagcac aggtaaagaag cacaacgccc tcgctctcca cctcccacc caatcgcgac 420
      gcacctcgcg gatcggtgac gtggcctcgc ccccaaaaaa tatcccgcgg cgtgaagctg 480
      acacccggg cccaccacc tgtcacgttg gcacatgttg gttatgttc ccggccgcac 540
55     caaaatatca acgcggcgcg gcccaaatcc tccaaaatcc cgccaaagcc cctggcgcgt 600
      gccgctcttc caccaggtc cctctcgtaa tccataatgg cgtgtgtacc ctcggtggt 660

```

EP 1 801 223 A2

```

5      tgtacgtggg  cggggttacc  tgggggtgtg  ggtggatgac  ggggtgggcc  ggaggaggtc  720
      cggccccgcg  cgtcatcgcg  gggcggggtg  tagcgggtgc  gaaaaggagg  cgatcggtac  780
      gaaaaattca  attaggaggt  ggggggcggg  gcccttggag  aataagcgga  atcgagata  840
      tggccctgac  ttggcttggc  tctcttctt  cttatccctt  gtcctcgcaa  ccccgcttcc  900
      ttctctctc  tctcttctc  ttctcttct  ttggtgtgtg  ggtgtgtccc  tgtctccct  960
      ctcttctc  ctctcttct  cctctctc  ttccccctc  tcacaagaga  gagagcgcca  1020
      gactctcccc  aggtgaggtg  agaccagtct  ttttgcctga  ttcgacgcgc  ctttcacgcc  1080
      gcctcgcgcg  gatctgaccg  ctctcctcgc  ctttctcgca  ggattcagcc  1130

10      <210>  19
      <211>  1230
      <212>  DNA
      <213>  Oryza sativa

15      <220>
      <221>  misc_feature
      <223>  PRO0171 - reversibly glycosylated protein RGP1

      <400>  19
20      tagtaccatt  cttccctcgt  gagcataaat  gtattcatat  aaaatagtaa  aatgtatcct  60
      cacaagatt  gtaagtatat  ctcgcaacta  taaatatgtt  gtcattttag  taacaattgt  120
      tcataaaata  gtaatcatgt  tctccataac  agtaaatgac  gaggcgttaa  tagtggttta  180
      ggttctcatg  attgtaaatt  ttgagtcgct  tgtagcggct  taagatatag  tagagagtat  240
      atctagtttt  atcaagacaa  acattgcgta  atgcctcgga  cctaataata  aagtaggaat  300
      tttaaccttt  gagaaactgt  aaccaattga  aactgcaagc  tttaaaaaaa  catctattgg  360
25      aagtgatatt  atatagacaa  aataagtttc  ttactcttac  tctctcagtt  tcaagttata  420
      aaatgttttg  gctttgggtc  aaatcaaact  tcttcaagtt  taatcaagtt  tatagaaaaa  480
      atagtaatat  ccaagataaa  tttattataa  aaatatattt  aattattatt  ttaataaaac  540
      taatttggtg  atgtaaatat  tactatattt  gtctataaac  ttagtcaaat  ttaaaacagt  600
      ttaactttga  ccaaagtcaa  aacatcttat  aacctgaaat  ggatggagta  tttgtttgtt  660
30      tctattttag  gaaacggccg  tttctttcca  ttgattttga  gataagcaga  gctttaaacc  720
      actgccacta  ttgtgcattt  catttgattt  aacactttta  ccccttatct  ccaataaaaa  780
      cgatattaag  atacccttat  cttttatcca  ccgcttgga  caaaccaaaa  aaaataaaaa  840
      ttcaaacctt  ctacactggt  acacacgttc  tctctttcca  tgcaccgaca  ggtctctccc  900
      agatccaacc  caaaataaat  ttggacgcat  cccaaaattc  ggcaaacata  tgacgcaaac  960
35      caaaacaaaa  taggcacaaa  ataataaat  actcctatct  aattaattat  acacaatttt  1020
      ttttaaaaaa  aaagcaaggc  aagcgaagca  aagcaaagaa  ggaaacgaat  aacaaagtcg  1080
      tcgtcctccc  ggagctcccc  ctctataaat  cgctcctcct  cccacccac  ccaaaccac  1140
      acacacctca  cacctcacca  ccatcacctc  ctctcctcct  tctcttctct  ccgcgcgcgc  1200
      gagatccagg  gagagggaga  gggagagatc  1230

40      <210>  20
      <211>  1234
      <212>  DNA
      <213>  Oryza sativa

45      <220>
      <221>  misc_feature
      <223>  PRO0173 - cytosolic MDH

      <400>  20
50      gtttggttgg  tgaccgcaat  ttgctatacc  aaaatccttag  acacagttga  attaagctac  60
      acttttattag  cacattggcc  cgtgcgttat  attgtcattt  tctagccaaa  gtttgccata  120
      attgtggcta  acaaatgtt  ggccacattt  tggctacgtt  cgataggaca  tgttcccaac  180
      ttctccttct  cgtttttcgc  gcgtacgtt  tttcaactg  ttaaacggtg  tgttttttgc  240
      aaaatatttt  ttacgaaag  ttgcttaaaa  aattatatta  atctattttt  tttaaaaaaa  300
      gtatgtaaaa  cttaattaat  ctacgcgtag  acgtgcttc  gttttacgtg  tcgggtaccc  360
55      aaccctcact  cccgaacaca  gcctttgtgt  ggtttactac  agttatagta  aagctagtct  420
      ccatccaaac  aatcctttag  tccatataac  ttctgtatact  ccaaaattcc  actcgttcta  480

```

EP 1 801 223 A2

```

cggacatcac taatacgaag atcaagtgga agatagatat ttttaatgac atgttatattt 540
cagtgaacac ttgaggtcct cagcatccac aaacacacat tttcgtagat aagttctgaa 600
atactccata cggcggttgt cagcatgtca tgatcgtcgt tacccaagga agaagaaaag 660
5 agtggcatct tctccacgcc agtgttccca acggagcatc ttttcttccc ccacacggca 720
tcgacgtcac acttttctggt gcaaaacttta ataattagtc caaaaacaaa aaaagaattt 780
cggccacatc tctctcccga acgccagggtg ggccccacct gcatcactga cagcctgtcc 840
ccacaacgcg cagtcgtgtc cccacctgtc aggatgttag cgtctccgtt gcaggtttcc 900
cagatcccat cgccgatctg tgggccagcg cccacgggtg cagccccgcg cacacctggc 960
tccaacccac ccaccccacg cgctccgtgg ccgacagcgt ggacccacct aggtggggcc 1020
10 caccgtcagt gggagatggg taggggagcc cccacgtggg agcaacgggg gttctccggg 1080
ctccccgtcg ccgcgaggtt aaataacggc caccggtttc cccctctctc gcaaaactca 1140
cccaaaagag cagcgtcgcc tctctctctc cccctaacc cctacgcttc cagaaccttc 1200
tcgaagctcc cgctccccc ccccttccgc tcca 1234

<210> 21
15 <211> 1553
    <212> DNA
    <213> Oryza sativa

<220>
20 <221> misc_feature
    <223> PRO0175 RAB21

<400> 21
25 gtcaccaccg tcatgtacga ggctgcttca ccactgcctc actgccacca gcgtctcccg 60
    ccgcgtgcaa tacaagaaga aacatcgaa c ggatataaa ygtaagacc actaccgatt 120
    taacctatca ttcccacaat ctaatccact tatttctctt cccatgatct tatcctctca 180
    tttctctcta ctacttttgc atttgttaga aacacaatga caccgtcgaa gaaagctggt 240
    ggagcacccgt agccagcaat caccaaaaca cagaggggag gaggtcggca gcggccatgc 300
    ggacggcgat gagacaacgc gacgcaaaaga gggaggagga cgttggcgat catgctggtg 360
30 ttggcggagg aggtcactgg ccatgcgaat gacagcgggg cagcgcaaca caaaaagggg 420
    ggaggatgcc ggcgaccacg ctagtaccat gaagcaagat gatgtgaaag ggaggaccgg 480
    acgaggggtg gacctctgcc gccgacgtga agagcgtgat gtgtagaagg agatgttaga 540
    ccagatgccg acgcaactta gccctgcaag tcaccgact gcatatcgct gcttgccctc 600
    gtcctcatgt acacaatcag cttgcttata tctccatact tgcgtttgt ttcccgtagc 660
    cgaaatagaa gaagacagag gtgggttttg ttggagagtt ttagtggtat tgtaggccta 720
35 tttgtaattt tggtgtactt tattgtatta atcaataaag gtgtttcatt ctattttgac 780
    tcaatgttga atccattgat ctcttggtgt tgcactcagt atgttagaat attcattccg 840
    ttgaaacaat ctgtggttaag ggttggaaca tttttatctg ttcggtgaaa catccgtaat 900
    attttcggtt aaacaatttt tatccgacag caccgtccaa caatttacac caatttggac 960
    gtgtgataca tagcagtcac caagtgaaac tgaccaccag ttgaaaggta tacaagtgta 1020
40 acttattcat ctaaaagacc gcagagatgg gccgtggccg tggctgcaaa acgacagcgt 1080
    tcaggcccat gagccattta ttttttaaaa aaatatttca acaaaaaaga gaacggataa 1140
    aatccatcga aaaaaaaaaa ctttctacg catcctctcc tatctccatc cagcgcgagc 1200
    actcatccaa accgtccatc cagcgacaca gtacacacac atagttatcg tctctcccc 1260
    cgatgagtca ccaccgtgt cttcgagaaa cgctcgccc gacaccgtac gtgcgccacc 1320
45 gccgcgcctg ccgcctggac acgtccggct cctctccgc cgcgctggcc accgtccacc 1380
    ggctcccgca cagctctccc tgtctccctc caccatgcc gtggcaatcg agctcatctc 1440
    ctgcctcctc ccggttata atggcggcc accacctca cctgcttgca caccacagca 1500
    agagctaagt gagctagcca ctgatcagaa gaacacctcg atctctgaga gtg 1553

<210> 22
50 <211> 1087
    <212> DNA
    <213> Oryza sativa

<220>
55 <221> misc_feature
    <223> PRO0177 - Cdc2-1

```


EP 1 801 223 A2

```

<400> 22
cagacaccta gaatatagac attcccaaaa aataatcact atgcatcagc atcactatac      60
atgacttggg tctagtgatg gaagtggata gttccactac ctacataaaa acccactact      120
5 agtttattac ttttcacatg atagcataaa atttaaagaa aaaataaaca gaagtggaat      180
aagcgaaaaa ccccgcttac ccgccccatt tacatcccta cttggatcct gcatgtcagt      240
aagatatcag aattatatgt tttagaatta tatgtttttt tgggaaggagg aaatcggatt      300
attagacgca acataccaag tggcgtatac ttggcttcac tctttccatc agagcaagcg      360
taaaagatca cgtattcacg tcacatggag taactgagcg aatttttttc atttttaaatt      420
10 ttttgttttt taatatattac ataaatatta taccggcgaa aatatattaca aaagtagacc      480
ctgctgcctt tctccttctc gagaagagcg gcagggtgat gtcagggaca gaaataaact      540
ccaaaaaatgc atttttggct gggcgaaaaat tgcacttacc cccttgctgc cctctacaaa      600
ggttgcaagg gacctcagtg caaaatacgc acaccttgcc gtcctccact tggacggcat      660
gggctatttc tgtaaatatt ttggatggta taatatctct gtaaataatta aaaaataaaa      720
15 atttaaaaat gaaaaaattc tatctgggct cccttctctc atctcacacg gccaccaca      780
caatcccgcc ccacatatatt cctgggcccc tttccgtgtg aatggagacg gccattggc      840
gcgcacatgc ggaaaagcgt acacacgatt cgaaatttga aatctcaaaa agcgcccggt      900
agagcgcgtc cctccaacg gctatcccca atacaaaaga tcaactgaat cccccccaaa      960
tcgaccaaac cctaaatcca cgcgcatctc acaccacca accagcgaga gagagatggc      1020
20 ggcgctccac caccaggcgg cggcggcgcc ggtgacgacg acgacggacg ggggcgagct      1080
gcgggcg      1087

<210> 23
<211> 1272
<212> DNA
25 <213> Oryza sativa

<220>
<221> misc_feature
<223> TC89946 (PRO0110)
30

<220>
<221> misc_feature
<222> (17)..(17)
<223> n = any nucleotide
35

<220>
<221> misc_feature
<222> (50)..(50)
<223> n = any nucleotide
40

<400> 23
tttgacgact gaatcgnggc tcgcctctgc ggcggccgct ctagattagn gtttcccctg      60
tctgttgtaa ttccggcacga gggctgatca agagctctta attagctagc tagtgattag      120
ctgcgcttgt gatcgatcga tctcgggtac gtagcaatgg cgtccaaggc gttcgcctctg      180
ttcctggccg tgaacctcgt cgtgctcggg gtggcaagcg cctgcggcgg cagcccgtcg      240
45 tgcccgacgc cgacgcgcgt gaccccga caacgcaacgc cgacgcgcgc gccgtcggcg      300
ttcgggaggt gccccgcga cgcgctgaag ctgggcgtgt gcgccaacgt gctgggcctg      360
atcaaggcca aggtgggcgt gcctccggcg gagccgtgct gcccgctgct ggaggggctc      420
gtcgacctcg aggcggcgggt gtgcctctgc acggccatca ggggcaacat cctcggaatc      480
aacctcaacc tccccatcga cctcagcctc atcctcaact actgcggcaa gaccgtcccc      540
accggttcca agtgctaagc agcgtgcata tgcaatgcct gcatgggttg atcctacgta      600
50 cggtgattag ttggctttga cgactcttga tttgatctgc ttgctgctct gtttatttgc      660
tactacgtta cgtacgtact ttgcatgcaa cgcaacgcat gatcgatcgt gcatgctggc      720
tgtttgtacg tatcacggta ccagtttgga ttctctctgt actctctcct ttgtcttctt      780
tgtagtactc ttattcccgc tatccgtacg tgcgcatttg ttgtaagggc cgggtgctagc      840
ttgtgtgccg gtaccaactt ctaataaagc tatgggtgga acttcaaaaa aaataaaaaa      900
55 aaaactggag ggggggcccg ggtccaattt agactataat gagtttaaca ccccgctcat      960
cggccgaaga taacaacacc gggcttgga aacctagact gcccaactaa tggacggaag      1020

```

EP 1 801 223 A2

acagactctt ggactgaaac tgaacgaaac aagaccaccc accccatcta accacagcca 1080
 cctaccgcca aagattccaa taatgtgaat cagtcggtaa tagaacactc ctcttgtacg 1140
 attttactgc ccgcgccacc cctcggtagc cacttatata tatcgggccg tagtaatttc 1200
 ctggttccgt cacttccctc atcgcacctg ctagtcgtgg cttacatacg tgcgtcctct 1260
 5 tattatcgag cg 1272

 <210> 24
 <211> 2425
 <212> DNA
 10 <213> Oryza sativa

 <220>
 <221> misc_feature
 <223> TC90358 (PRO0005)

 15 <220>
 <221> misc_feature
 <222> (1558)..(1558)
 <223> n = any nucleotide

 20 <400> 24
 cccacattga ataattatit taaataatit aagttttitit tttttggctt tagatatatt 60
 cccaatcccc aacctcccaa taatccgato tctcccagtt ctgttcggat caaggctgtg 120
 tcgatcgcaa aaaagaaaaa aaaaacaatt tccttttggg gtggttcacg tgttgatcac 180
 ttctttgttt cccgcgtttt gttggggatt cgattttcgg gtttaagattt tctacacgat 240
 25 ygctttgaac ttggctcaga gcgcgcgcgc gcgcgcgcgc ttcgcgaccg ccggtgatgc 300
 gcggcgagct gcttcgggtg tcgccatgcc gtcgtcgtcg tcgtcggcca cgacgagcct 360
 gaggatgaag aggcagggcg cgtgcgagcc ggtggcgtgc cgggcggtgg ccaggcacgt 420
 gcggcggcgc gcggcgagca gcaggaggaa cggcgtgccg gtgttcgtga tgatgccgt 480
 ggacacgggt agcaagtgcg ggagcgcgt gaaccggagg aaggcgtgg cggcgagcct 540
 30 gcggcgctg aagagcgccg gcgtggaggg gatcatggtg gacgtgtgtt ggggcatcgt 600
 ggagagcgag ggccccggcc ggtacaactt cgacggctac gtggagctca tggagatggc 660
 ccgcaagacc ggctcaagg tccaggcgt catgtccttc caccagtgcg gcggcaacgt 720
 cggcgactcc gtcaacatcc cgtcccagc gtgggtgttg gaggagatgg agaaggacaa 780
 cgacctcgcc tacaccgacc aatggggacg ccgcaacttc gactacatct ccctcggctg 840
 cgacgccatg cccgtcttca agggccgcac gccgcgtcag tgctacaccg acttcatgcg 900
 35 cgcttccgc gaccacttcg cctccttct cggcgacacc atcgtcgaat tccaagtcgg 960
 catgggcccc gccggcgagc ttcggtaccc gtcctacccg gagagcaacg gcacctggag 1020
 gttccccggc atcggcgctt tccaatgcaa cgacaggtac atgcgtagca gcctgaaggc 1080
 ggccggcgag gcgaggggca agccggtagt ggggccacgg cgggccgacg gacgcccggc 1140
 gctacaacaa ctggccggaa gacacgggtg tcttccgcg cgaactgcgc ggggtggagca 1200
 40 ccgagtacgg cgagttcttc ctgtcgtgtt attcgcagat gctgctggag cacggcgagc 1260
 gcgtgctgtc gggcgcgacg tccgtgttcg gcgacggcgc cggcgccaag atctcgttca 1320
 aggtggcccg catccactgg cactacggca cgcggtcgca cgcgcccggag ctacacggcg 1380
 ggtactacaa cagcgcgac cgcgagcggc tacctcccga tcgcgcgcgt gctggcgcg 1440
 cacggcgccg tgcctcaactt cacctgcgtg gagatgcgcg accacgagca gccgcaggag 1500
 45 gcgcagtgca tgcccagggc gctcgtcagg caggtggccg ccgcggcgcg cgcggcgnga 1560
 cgtcgggctc gccggggaga acgcgctgcc gcggtacgac ggcacggcgc acgaccaggt 1620
 ggtcgcggcc gccgcggacc gcgcggcgaa ggaccggatg gtcgccttca cctacctccg 1680
 gatggggccc gacctcttcc acccggaaca ctggcgcccg ttcgtcgctt tcgtccgccc 1740
 catgtccgag tccggctcgc cgcgggaggc cgcgagagc gccgcgcacg gcgtcgcgca 1800
 50 ggccaccggc tcgctcgtgc acgagggcgc ggtcgcgctc cggagctagc accggtcaga 1860
 cgctcatata caccgtcgcc tcgaggtcgg attccgatgt gggatcatto gatctccctt 1920
 ttttttttct tctttttgcc attttgtaca gccttttggg gagcttttga ttttgtcttt 1980
 ttgtctcggg aggaataaccg ctctggaggt cgaagagagc gtcattttcc tcccgttgaa 2040
 gatcacgaat catttacgtt agagatgatg taattaagca gggaggggag gggaaacacac 2100
 acacactggc actcaaaagt tgtgtcacg cttggggaat atatccattt ccagccaaaa 2160
 55 aaaaaacgca gaaatgcgtt gtgttcttgc gctctggttc gttgctgctg tgggtcagat 2220
 tcagctggtg aaaaaactac agtactactg aaactgaaac tactagagcc tagagggaga 2280

EP 1 801 223 A2

	ttaagctaag	ttaattgcac	gagtaattac	tccacggttg	tgtttaggg	ctacgtcggc	2340
	agattttgct	ttctggtaga	tccctaacct	tatgtttgtt	gggaatttta	taaaggagct	2400
	aagtttgctt	attgatttgc	aatct				2425
5	<210>	25					
	<211>	3410					
	<212>	DNA					
	<213>	Oryza sativa					
10	<220>						
	<221>	misc_feature					
	<223>	TC83635 (PRO0009)					
	<400>	25					
15	ccatggacac	cgctccgtc	accggtggcg	agcacaagg	gaaggagaag	acgtgccggg	60
	tgtgcggcga	ggaggtggcg	gcgagggagg	acgggaagcc	gttcgtggcg	tgcgccgagt	120
	gcggcttccc	ggtgtgcaag	ccctgctacg	agtacgagcg	cagcgagggc	acccagtgtc	180
	gcccccagtg	caacacccgc	tacaagcgcc	acaaaagggtg	cccacgggtg	gaaggcgacg	240
	aggacgacgy	cggcgacatg	gacgacttcg	aggaggagtt	ccagatcaag	agccccacca	300
	agcagaaacc	ccccacgag	ccggtcaact	tcgacgtcta	ctcggagaac	ggcgagcagc	360
20	cggcacagaa	gtggcgccct	ggaggcccg	cgctctcttc	cttcaccgga	agcgtggctg	420
	ggaaggatct	ggagcaggag	agggagatgg	aggggtggcat	ggagtggaa	gacaggatcg	480
	acaagtggaa	gacgaagcag	gagaagcggg	gcaagctcaa	ccgcgacgac	agcgacgacg	540
	acgacgacaa	gaacgacgac	gagtacatgc	tgctcgcgga	ggcgaggcag	ccgctgtgga	600
	ggaaggtgcc	gatcccgctg	agcaagatca	acccgtaccg	gatcgtgatc	gtgctccggc	660
25	tggtggtgct	ctgcttcttc	ctcaagttcc	ggatcacgac	gccggcgatg	gacgcggtgc	720
	cgctgtggct	ggcctcggtg	atctgcgagc	tgtggttcgc	gctgtcgtgg	atcctcgacc	780
	agctgcccc	gtggctcgcc	gtgacgaggg	agacgtacct	ggaccggctg	gccctccggt	840
	acgagcgcg	cggcgagccg	tgccgcctgg	ccccgatcga	tttcttcgtc	agcacgggtg	900
	acccgctcaa	ggagccgccc	atcatcaccg	ccaacaccgt	gctgtccatc	ctcgccgtcg	960
30	actaccccg	cgaccgcgtc	tctgtctacg	tctccgacga	cggcgcgctc	atgctgctct	1020
	tcgacacgct	ctccgagacc	gccgagttcg	cccgcgggtg	ggtcccttc	tgcaagaagt	1080
	tcaccatcga	gccccgcgcc	cccagattct	acttctccca	gaagatcgac	tacctcaagg	1140
	acaaggtcca	gcccaccttc	gtcaaagaac	gccgcgccat	gaagagagag	tatgaggagt	1200
	tcaaggtgag	gataaacgcg	ctggtggcga	aggcgagaa	gaagccggag	gaagggtggg	1260
35	tgtatcagga	agggacgcca	tgcccgggga	acaacacgag	ggaccacccg	gggatgatcc	1320
	aggtgtacct	ggcgagccag	ggcgcgctcg	acgtcgaggg	cagcgagctg	ccgcggctgg	1380
	tgtacgtgtc	ccgcgagaag	cggcccggct	acaaccacca	caagaaggcc	ggcgccatga	1440
	actccctcgt	tcgctgtctc	gccgtgttta	ccaacgcccc	cttcatectc	aacctcgact	1500
	gcgaccacta	cgtaacaac	agcaaggccg	tccgcgaggg	catgtgtctc	ctcatggaca	1560
	agcagctcgg	ctaagaagctg	tgctacgtcc	agttccccca	gcgcttcgac	ggcatcgacc	1620
40	gccacgatcg	ctacgccaac	cgcaacaccg	tcttcttcga	catcaacatg	aaggggctgg	1680
	acgggataca	ggggccgggtg	tacgtgggga	cggggacggt	gttcaacagg	caggcgctgt	1740
	acggatacga	ccgcgcgcgg	ccggagaaga	ggccgaagat	gacgtgcgac	tgctggccgt	1800
	cgtggtgctg	ctgctgctgc	tgcttcggcg	gggggaagcg	cggcaagtcg	cacaagaaca	1860
	agaaggcgcg	cggcgggcgc	gagggcgcg	gcctcgacga	gccgcgcgc	gggtgctcg	1920
45	ggttctacaa	gaagagagc	aagaaggaca	agctcgcgcg	cggcgcgcg	tcgctcgccg	1980
	gagggaaaga	agggatccgg	aagcaccagc	cggggttcga	gctggaggag	atcgaggagg	2040
	gcctcgaggg	gtacgacgag	ctggagcgct	cgctcgctcat	gtcgagaag	agcttcgaga	2100
	agcggttcgg	ccagtcgccg	gtgttcacat	cctccaccct	cgtcgaggac	ggcgccctcc	2160
	cccagggcgc	cgcgcgcgac	cccgcgcgcc	tcatcaagga	ggccatccac	gtcatcagct	2220
	gcggctacga	ggagaagacc	gagtggggca	aggagattgg	gtggatctac	gggtcgggtg	2280
50	cggaggacat	cttaacgggg	ttcaagatgc	attgcccgtg	gtggaagtcg	gtgtactgca	2340
	cggcgcgag	ggcgccattc	aaggggtcgg	cgcccatcaa	cctgtcggat	cgtctgcacc	2400
	aggtgctccg	gtggcgctc	ggctccgtcg	agatcttcat	gagccgccat	tgcccgctct	2460
	ggtaccctat	ggcgccgcgc	tcaagtggct	cgagcgcttc	gcctacacca	acaccatcgt	2520
	ctaccccttc	acctccattc	ccctcctcgc	ctactgcacc	atccccgcgc	tctgcctcct	2580
55	caccggcaag	ttcatcatcc	ccacgcttaa	caatttgggc	agcatatggg	tcatagcgct	2640
	tttctgtcgc	atcatcgcca	cgggggtgct	ggagctcgcg	tggaagcggg	tgagcatcga	2700

EP 1 801 223 A2

```

5      ggactggtgg aggaacgagc agttctgggt gatcgggcgc gtgtcggcgc acctgttcgc 2760
      cgtgtttccaa ggcttctca aggtgctcgg cggcgtggac accaacttca cggtgacgtc 2820
      caaagccgcc gccgacgaag accgacgcgt tcggcgagct ctaactgttc aagtggacga 2880
      cgctgctggt gccgccgacg acgctgatca tcatcaacat ggtggggatc gtcgccggcg 2940
      tgtcggaagc cgtgaacaac gggtagcggg cgtggggccc gctgttcggg aagctcttct 3000
      tctccttctg ggtcatcctc cacctctacc ccttctcaa ggggctcatg gggaggcaga 3060
      accggacgcc cacaattgtc gtgctctggt ccaacctcct cgctccatc ttctcctcgc 3120
      tctgggtcag gatcgacccc ttcattccca agcccaagg ccccgctctc aagccatgcg 3180
      ggggtctcgt ctgagctgct gctgctactt ctctgtgtct ctgcattttg caagagggat 3240
10     gaccggatgg atgattcttg ttgtatggag tattttgact tgttcatgta caagtttttg 3300
      tgagtgggat aaaagtgttt tgggggtaaa atttgtaaga actgaggtgg agattatact 3360
      cgaatttaag aacaattgtt tttgaatttt cttttaagat ttttgggagt 3410

      <210> 26
      <211> 602
15     <212> DNA
      <213> Oryza sativa

      <220>
      <221> misc_feature
20     <223> TC83117 (PRO0058)

      <400> 26
      cccccctc gaggttcgac ccaactcgtc gctgacgggt agttccaagg gaaagaagaa 60
      atggaggctt cagcgaaggt gttctcggcc atgcttctca tgggtgctgt gcttgacgac 120
      actggtgaga tgggcgggcc ggtgatggtg gcggaggctc ggacgtgcga gtcgcagagc 180
25     caccggttca agggcccggt cgcccgcgaag gcgaactgcg ccagcgtatg caacacggag 240
      gggttccccg acggtactgt ccacggcgct cgccgcgct gcatgtgcac caagccctgc 300
      ccctgatcga tgaaccagca gctagcgcag cagcttgtgc cgccacctcg cgcatgtgtc 360
      atcgtgtcga tcgatcggat cctagctgcc ctatgaatga ataaaagtgt gtggcttatg 420
      cgtggttttc tcttgagaa ctttggtttt tgtggtgtta agttcgatcg ttttgtgcat 480
30     ccaccatcca tccatcctcc cattctgctt gttctaaggt tatactacta cttgagaagg 540
      tgatgcaatt gtgctcaaca gtttattaat acttcatccg ttttaaaatg tttgaccccg 600
      tt 602

      <210> 27
      <211> 1170
35     <212> DNA
      <213> Oryza sativa

      <220>
      <221> misc_feature
40     <223> TC89913 (PRO0061)

      <220>
      <221> misc_feature
      <222> (15)..(16)
45     <223> n = any nucleotide

      <220>
      <221> misc_feature
      <222> (1162)..(1162)
50     <223> n = any nucleotide

      <400> 27
      aattcgccac gagannaaaa ggaaaaaaa acaaacacac ccaagccaaa taaaagcgac 60
      aatgggatcg ctaccacca acatcgtcct cgccgtcgcc gtgggtggcag cgctgggtcg 120
      cggggggtcg tgcggccgcg ccaagtgccc accggggccc aacatcacga ccaactacaa 180
55     cgcccgtggt ctccccgcca gggccacctg gtacggccag ccctacggct ccggctccac 240

```

EP 1 801 223 A2

```

cgacaatggt ggcgcgtgcg ggatcaagaa cgtcaacctg cctccctaca acggcatgat 300
ctcctgcggc aacgtcccaa tcttcaagga cggcagggga tgcggctcat gctacgaggt 360
gaagtgtgag cagccggcgg cgtgctcgaa gcagccggtg acggtgttca tcacggacat 420
gaactacgag cccatctcgg cgtaccactt cgacttctcc ggcaaggcgt tcggcgccat 480
5 ggcttgcggc gggaaggaga ccgagctccg caaggccggc atcatcgaca tgcagttcag 540
gaggggtgcg tgcaagtacc ccggcggcca gaaggtcacc ttccacgtcg agaagggtc 600
caaccccaac tacctcgccg tgctcgtcaa gtctcgtcgc gacgacggtg acgtcatcca 660
gatggacctc caggaggccg gattgccagc gtggaggccc atgaagctgt cgtggggcgc 720
catctggagg atggacaccg ccacgccact caaggcacc ttctccattc gcgtcaccac 780
10 cgagtcggcg aagagcctca tcgccaaaga cgtcatcccg gtcaactgga tgccagacgc 840
catctacgta tcaaacgtcc agttctattg agatcggacg gaaacgatcc tcctaattta 900
tttccttatt aatttggtca aatggtttcc ttctataacc tatatttttc ccgttggttag 960
aaatggttcc atttctctct acagcttact ttaagatagt tgcgcttgta tatctgcgcc 1020
atcttgtaag ttgtaagatg ctgaagaaca ctatgaattc tgagcatctg attctccggg 1080
15 aagatttact atgataaaca acagtttgat ttactatgtg tgtccccttg tttattgtat 1140
gctatcctaa tacttatgaa angttttgat 1170

<210> 28
<211> 861
<212> DNA
20 <213> Oryza sativa

<220>
<221> misc_feature
<223> TC89985

25 <400> 28
ccacgcgtcc gccacgcgt ccgcgatcag cagcagcagc agcttgcaaca ctcgagctta 60
gcttagcttt tgcaagagag atcgagctag agatggagaa gtcgagcaag atgatggcgg 120
tgccggcggt gctggtgctc gcggtggtcg gcgcggcgga ggcgaggaaac atcaaggcgg 180
30 cggcgggcgg ggccggcgag agcaaggaca cgggtggtgca gccgacgacg ttcccgccgt 240
tcgaccgctt cgggagcgcg gtgccggcgt tcggcgcat gcccggcagc agcatcccgg 300
ggttcagcct ccccggcagc agcggctcca ccccggcgg cctcggcggc ttccggcagca 360
tgcccatggt cggcggcctc ggccggcggt cacctggcct cggcggcggc atgcccggt 420
ccccgcgcgc gcgcgacaag caggccaaga agccatgaga gacctcgccg tcgcccggcg 480
35 cgtcgccgct gctgcgcggg taatgtgctc tatgtagcgc acggcggtgc atgcaatatg 540
gatggctata tgacgcgcgc gcgttatatc ttcatatgtg cagttagctt gcaactgtgtc 600
tagctagcgt tctattatga gtagtgtctc ttctatctct tttctttaca tgcatttgga 660
ggaggtattt tctatctgtt tgttggttgg ttgtgtttgt ttgttttaat taggtccctt 720
cttatatttt gtgttttaat taagtctgtg atcatgtagt agtactacca ctgtttcgag 780
ctcgaggcat gaataatgct aaatgtgatc attattgtgt tattgtatgg tgatggctat 840
40 atataattact atctctgctt c

<210> 29
<211> 1252
<212> DNA
45 <213> Oryza sativa

<220>
<221> misc_feature
<223> TC89891 (PRO0081)

50 <220>
<221> misc_feature
<222> (5)..(5)
<223> n = any nucleotide

55 <400> 29
cccangcgtc cgaaccaatc gactcgcacc accaccagca gctcaagcag caacagctca 60

```

EP 1 801 223 A2

```

aacggaggaa gatctcatcg ccatgacgac cggcaatggc gacgcaccgg tgatcaagaa 120
cgcccacagc gacatcgaca gcaccaacaa gacgctgctc aagagcgacg ccctgtacaa 180
gtatgtcctg gacacgacgg tgctgccacg ggagccggag tgcattgcgc atctgcgcct 240
5 catcacggac aagcaccagt ggggggttcat gcagtcgctc gcggatgagg cgcagtgtcg 300
gggatgctgc tgaagatggc cggagcgaag aggacaatcg aggtgggtgt cttcaccggc 360
tactcgctgc tggcgacggc gctggcgctg ccggaggacg ggaaggtggt ggcgatcgac 420
ccggacaggg agagctacga gatcggcgcg ccgttcttgg agaaggccgg ggtggcgcac 480
aaggtggact tccgcgaggg gaaggggctg gagaagctgg acgagctgct cgccgaggag 540
10 gcggcggcg ggcgcgaggc ggcgttcgac ttcgcgttcg tggacgcgga caagcccaac 600
tacgtcaagt accacgagca gctgctgcag ctggtgcgcg tcggcgggca catcgtgtac 660
gacaacacgc tgtgggcccg caggtggcg ctgccgcccg acacgccgct gtcggacctg 720
gaccggaggt tctccgtcgc catcagggac ctcaactcca ggctcggcg cgaccgcgc 780
atcgacgtct gccagctcgc catcgccgac ggcatcacca tctgccgccc cctcgtgtga 840
ggtcgagacc gagaccttac cggccgatcc atccatcgct ctgcgctgat taattaacct 900
15 gtgttgctgt actcttctac tgcataact atactattac ttccttaatt gccgcttaaa 960
ttttcctata cgtgtttcaa tcaatgagat tattatattc ttcgagcatg agagagacgg 1020
agttgtatgg acatttgyat atggttgta ctgtactaca tgytgataag tgcaacatct 1080
ctttccatgg ttgctactct actcaccgtg tcatgttggt tgcggatttt gatctcatct 1140
gcaagatgga ctactggggc ccaaaatgga acagactggg ccctcgatcc tgcaggagct 1200
20 tgcacctgtt gcaagggcct ttttaactgg ctaactaggt gggttaagtag gg 1252

```

```

<210> 30
<211> 671
<212> DNA
25 <213> Cryza sativa

<220>
<221> misc_feature
<223> TC89670 (PRO0091)

30 <220>
<221> misc_feature
<222> (3)..(3)
<223> n = any nucleotide

35 <220>
<221> misc_feature
<222> (14)..(14)
<223> n = any nucleotide

```

```

40 <400> 30
gcnggcttcg gcangagttc aaacattata gttgaagcat agtagtagaa tcctacaaaa 60
atgaagatca ttttcgtatt tgctctcctt gctattgttg catgcaacgc ttctgcacgg 120
tttgatgctc ttagtcaaag ttatagacaa tatcaactac aatcgcatct cctgctacag 180
caacaagtgc tcagcccatg cagtgaagtc gtaaggcaac agcatagcat agtggaacc 240
cccttctggc aaccagctac gtttcaattg ataaacaacc aagtcatgca gcaacagtgt 300
45 tgccaacagc tcaggctggt agcgcaacaa tctcactacc aggccattag tagcgttcag 360
gcgattgtgc agcaactaca gctgcagcag gtcgggtgtg tctactttga tcagactcaa 420
gctcaagctc aagctttgct ggccttaaac ttgccatcca tatgtggtat ctatcctaac 480
tactacattg ctccgaggag cattcccacc gttgggtgtg tctggtactg aattgtaata 540
gtataatggt tcaaatgtta aaaataaagt catgcatcat catgcgtgac agttgaaact 600
50 tgatgtcata taaatctaaa taaaatcacc tatttaataa gcattcatgt atgagttcca 660
ttatcatagc t 671

```

```

<210> 31
<211> 436
<212> DNA
55 <213> Cryza sativa

```

EP 1 801 223 A2

```

<220>
<221> misc_feature
<223> TC89883 (PRO0095)

5  <400> 31
    cctcgagggt cgacccacgc gtccgctctc ctctcttctc tcgccctcac cgctcgccga      60
    gggtgcgcgc tccttgcttc ctccgctcct tgcgcgcgcg ccgcgacgag tcgcggggag      120
    gggcgcgcat ctccatctcc atctgaggcg aggagagcag gggaggtagg gggatcctgg      180
    tgaggtttgt gattactgga caatagaaat atttacacaa tatggctggc ggctctgctg      240
10  atgcagtgac caaggagatg gaggcgctac tcgttggaaca aaatccaaat gcggttagtg      300
    gaaaaacatg cgagacctca tcaaaagaag gcaaagttgc agatagcaat ggatctcatt      360
    cttcaccacc agaagatgat gatgatgaag cgcaagggga tgggccatct caagattgga      420
    ggatccagaa gctttc                                     436

15  <210> 32
    <211> 860
    <212> DNA
    <213> Oryza sativa

20  <220>
    <221> misc_feature
    <223> TC90434 (PRO0111)

    <220>
    <221> misc_feature
25  <222> (1)..(1)
    <223> n = any nulceotide

    <220>
    <221> misc_feature
30  <222> (10)..(10)
    <223> n = any nulceotide

    <400> 32
    nagggtaan attaccggag tattttttgca aaggaggtaa tcaaagttcc aatacgaaat      60
    cgcggtcgta gtagtacaat acaaagacga gtacacggag cgcgtaaaact aataaggaaa      120
35  aattaaacgt cgcgagagaaa taatagccga actggatgaa gatgagcagc actgcctctt      180
    gcctagccta gccatcatg gcgaggccga cggccccgac cagcaggccc atcaccgaac      240
    yggcctcgtt gccgttggtc ccgcccgtgc tgcctctcga ctctgtctgc gtcgtctctg      300
    gcgtcgtggt cgcgtccggc gtcgacgagg gcgtgtccat gccgggggtcc gatgacggcg      360
    tggcggggcgt cgcgttggtg ggcggggacg acgacgccgt cgggggtggg gtggtgccgg      420
40  ccgccgcgga gaccgtgacg gcgagcttca tgccgcgga gcagtggccg ctggtgccgc      480
    agatgaagta gcgggtgccg ggcttggtga gcgcgatctt ggtgttctgg tcgctgtagg      540
    actggatcga gttgctggcg gacacgcgct gtagtcagcc gagctcacct ccgccaccgt      600
    gtgcatcatg ctgtactgga acacgagcga gtcaccaacg ctgaagggtt tgcctcttcg      660
    ccaggtatcg tagtccacgc cactgctcca gccggatgtg tcgccgacgg tgtagtccga      720
45  ggcgaaagcc ggcgcaacgg cggcgaggag tagcaccacc agacctgcag ctgcaagtcc      780
    atgtactcca gccatgatgg cagagttaat tagcaaacgc gaactgatta gagccgtact      840
    agtactggtg gccctcgtgc                                     860

    <210> 33
    <211> 1167
50  <212> DNA
    <213> Oryza sativa

    <220>
    <221> misc_feature
55  <223> TC83072 (PRO0116)

```

EP 1 801 223 A2

```

<400> 33
aggaaaagaa gaaaaaagat cctgtgaacc ctacgaaact accgaagcga acggaaggca 60
ggaatcggcg gcggcggcgc cggcggcggt ggggagaagc catggagcgc ctgcagcgcga 120
5 tcttcggcgc ctccggcatg gggcagccgc cgtcggactc gccgctgctc gactcctccg 180
agcagggtcta catctcctcc ctccgccctcc tcaagatgct caagcacggg agggccggcg 240
tgccgatgga ggtgatgggg ctgatgctgg gggagtctgt cgacgactac acggtcaggg 300
tggtcgacgt cttcgccatg ccgcagagcg ggaccggggt cagcgtcgag gccgtcgacc 360
atgtcttcca gaccaacatg ctgcacatgc tcaagcagac cgggaggcca gaaatggtgg 420
10 taggttggtta ccattcccat cctggatttg gttgctggct ttcaggagt t gacatcaata 480
ctcaacagag ttttgaagct ttaaacccca gggcagttgc cgtcgtgata gatcccatcc 540
aaagtgtcaa ggggaaagt t gtcattgatg catttcgcct tattaaccct cagaccatga 600
tgcttggtca ggagccacga cagacaacat caaatggttg gcacctaaat aagccatcta 660
ttcaggctct tattcatggg ctgaacaggc actactattc aattgcaatc aattaccgga 720
15 aaaatgagct tgaggaaaag atgttactga acttgacaaa aaagaaatgg accgatggat 780
tgattctgaa gaggtttgac actcattcaa agaccaatga gcagactgtt caggaaatgc 840
tgaaaccttc tatcaagtac aacaaggcgc tgcaagagga ggtatgagctg ccgcctgaga 900
aattagcgat agcaaattgt ggacggcaag atgctaagaa gcacttgga gagcatgtct 960
ccaatttgat gtcatacaac atagttcaga cgctaggaac catgctcgat acagttgtat 1020
tttagatcac tactgctgtt atcccaacac tgtaccaga gctcgtttat tttttatttt 1080
20 tttatgttta tcgaagccta ccataattca gtgaacttaa cgccagttac atttgggtta 1140
tgaaagctta ccacttgaca acttcat 1167

<210> 34
<211> 871
25 <212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
30 <223> TC90038 (PRO0117)

<400> 34
cctagctcct cccgccgcgc cgcgccgcgc cgcgccgcgc tctccactcg agagaccag 60
ccgccgcgcgc cgcgccgcgc gccatgtcgc tgatcgccgc ggaggacttc cagcacatcc 120
35 tgcgtctgct gaacaccaac gtcgatggga agcagaagat catgttcgcgc ctacactcca 180
tcaaggggtgt cggccgcagg ttctccaaca tcgcctgcaa gaaggccgac atcgacatga 240
acaagagggc cgggtgagctt acgccggagg agctggagcg gctgatgacc gtggtggcga 300
acccgcggca gttcaagtg cccgactggt tcctcaacag gaagaaggac tacaaggacg 360
ggaggttctc ccaggttgtc tccaacgcgc tcgacatgaa gctcagggat gatcttgaga 420
ggctcaagaa gatcaggaac caccgtggtc tgaggcacta ctggggcctc cgtgtgcgtg 480
40 ggcagcacac caagacaacc ggaaggagg gtaagactgt cgggtgtgtcc aagaagcgat 540
aagcctaaga accaccgag acttgatgaa gcgtttcgtt ggggtgatgtt ttgccctagg 600
ataatatatt gcagctatgg aaccttgctg taatgtatct tgaagagtgt ctttggaac 660
taagagtaat ttacttttct tgaaactatt gcagtattga ctcttgttt attgcttttc 720
tccactttct tctaccact taaaactatt gcagtatcga ctcttgttt attgctattc 780
45 tccactggct tctgccttaa ttttgatgt tgcatgcgct gtgtatctgg ttcattgtgat 840
gtaccatgg cagctttgat gcattgggat t 871

<210> 35
<211> 1245
50 <212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<223> TC82936 (PRO0122)
55 <400> 35

```


EP 1 801 223 A2

acgcgggccaa aacgtaccct tgtgactaca cccgcttcgc ttcctccctt ctctaagccg 60
 gggaagctaa gccatggcgt ccgtcaccgc ccgcaccccg gtcgcagccc tccgctcgtc 120
 ggcgtcgctc aagtctacct tcctagggca atcctccacc cgcctcgccc gcgcaccgac 180
 5 tacgaggcgt aatgttcggg cggaggccaa gggagagtgg ctccccggcc tcccttctcc 240
 cacctacctc aacggcagct tgccaggcga taacgggttc gaccggttg gtctggcgga 300
 ggacccggag aacctgcggt ggctcgtgca ggcggagtgg tgaacgggcg gtggcgatg 360
 ctgggggtgg ccgggatgct gctgcctgag gtgctgacga agatcgggtt gatcgacgcg 420
 ccgcagtggc acgacgccgg caaggccacc tacttcgcgt cgtcgtcgac gctgttcgtc 480
 atcgagtcca tcctgttcca ctacgtggag atccggcggt ggcaggacat caagaaccct 540
 10 ggctgcgtca accaggaccc catcttcaag agctacagcc tcccgccgca cgagtgcggc 600
 taccgccgga gcgtcttcaa cccctcaac ttcgagccca ccctcgaggc caaggagaag 660
 gagctcgcca accggaggct ggcgatgctg gcgttcttgg gggtcctggg gcagcacaac 720
 gtgacgcaga aggggccctt cgacaacctg ctgcagcacc tgtctgaccc gtggcacaac 780
 accatcatcc agacgtgtc aggtgagcgt tgtgatcgat ttcacaggg ccagggcac 840
 15 tcaaggagct tgatgagttc aggtcggtga aaccgatgat tgggcgatgg aagatgttct 900
 cttcttgttt cttctttttt tttttgtgga gtatgcatgt ataagatgtt aatgaattgg 960
 ggggagagaga gagagagaga tggatgtgat gagattcaga cttactgtgt gtgtgtgtgt 1020
 aattgtttcc tgcatgcatg gatctggatg catgggtgag ggggtgagtt gagtgtgtga 1080
 tttctgatgt acagtactac agggggataa actatctcat ggtagcagca gtgttctagc 1140
 20 tatctcatgg tctcgatctt aattatgggt gataaactac gcttaattgc ttgtcaagtg 1200
 cttcatttgc gcattgatcc agtattgcgt atcgattcaa agacc 1245

 <210> 36
 <211> 1416
 <212> DNA
 25 <213> Oryza sativa

 <220>
 <221> misc_feature
 <223> TC89839 (PRO0123)
 30
 <400> 36
 cccacgcgtc cgcacacgcg tccgggacac cagaaacata gtacacttga gctcactcca 60
 aactcaaaaca ctcacaccaa tggtctctcca agttcaggcc gactcctgc cctctgtctt 120
 ctctgtccccc aagaagggta acttgagcgc ggtgggtgaag gagccggggt tccttagcgt 180
 35 gagcagaagg ccaagaagcc gtcgctgggt gtgagggcgg tggcgacgcg gcgggccggt 240
 ggcgagcccc ggcgcgggca cgtcgaaggc ggacgggaag aagacgctgc ggcagggggt 300
 ggtgggtgat accgcgcgt cgtcgggggt cgggctcgcg gcggcgaagg cgtctggcgg 360
 agacggggaa gtggcacgtg gtgatggcgt tccgcgactt tctgaaggc ggcgacggcg 420
 gcgaaggcgg cggggatggc ggccggggagc tacaccgtca tgcacctgga cctcgcctcc 480
 40 ctgcacagcg tccgccagtt cgtggacaac ttccggcgct ccggcatgcc gctcgacgcg 540
 ctgggtgtgca acgccgcaca tctaccggcc gacggcgcg caaccgacgt tcaacgcgga 600
 cgggtacgag atgagcgtcg ggggtgaacca cctggggccac ttcctcctcg cccgcctcat 660
 gctcgacgac ctcaagaaat ccgactaccc gtgcgcggcg ctcatcatcc tcggctccat 720
 caccggcaac accaacacct tcgccggcaa cgtccctccc aaggccgggc taggcgacct 780
 ccgggggctc gccggcgggc tccgcgggca gaacgggtcg gcgatgatcg acggcgcgga 840
 45 gagcttcgac ggcgccaagg cgtacaagga cagcaagatc tgtaacatgc tgacgatgca 900
 ggagttccac cggagattcc acgaggagac cgggatcacg ttcgcgtcgc tgtaccggg 960
 gtgcatcgcg acgacgggct tgttcgcgca gcacatccc cgtttccggc tgcgtttccc 1020
 gccgttccag cgttcgtga cgaaggggtt cgtgtcggag gcggagtccg ggaagcggct 1080
 ggcgcaggtg gtggcgaccc cgagcctgac caagtccggc gtgtactgga gctggaacaa 1140
 50 ggactcggcg tcgttcgaga accagctctc gcaggaggcc agcgaccccg agaaggccag 1200
 gaagctctgg gacctcagcg agaagctcgt cggcctcgtc tgagtttatt atttaccat 1260
 tcgtttcaac tgttaatttc ttcgggggtt aggggggttc agctttcagt gagagaggcc 1320
 tgtcaagtga tgtacaatta gtaatttttt tttacccgac aaatcatgca ataaaaccac 1380
 aggcctacat tatcgatttg tccacctaaa ttaagt 1416
 55
 <210> 37
 <211> 1149

EP 1 801 223 A2

```

<212> DNA
<213> Oryza sativa

<220>
5 <221> misc_feature
  <223> TC85888 (PRO0133)

<400> 37
10 cttctacttc tatcatacca aacaaactag cttaatttgc attgcatcac attgccggcc 60
   gccatgagag ctctcgctct cgcggtggtg gccatggcgg tgggtggccgt gcgcggcgag 120
   cagtgcggca gccaggccgg cggcgcgctc tgccccaact gcctctgctg cagccagtac 180
   ggctgggtgc gctccacctc cgattactgc ggcgcggtc gccagagcca gtgctccggc 240
   ggctgcggcg gcggcccgcac cccgccctcc agcgggtggcg gcagcgcgct cgctccatc 300
   atatcgccct cgctcttcga ccagatgctg ctccaccgca acgaccaggc gtgcgcgct 360
15 aagggcttct acacctacga cgcttcgctc gccgcgcgca acgcctaccg ggacttcgcc 420
   accaccgcgc acgcccgcac ctgcaagcgc gaggtcgccg ccttctctgg gcagacgtcc 480
   cagcagacca ccggcggtcg gccacggcg cccgacggcc cctactcctg gggctactgc 540
   ttcaaggagg agaacaacgg caacgcccc acatactgcg agcccaagcc ggagtggccg 600
   tgcgcgcgcg cgaagaagta ctacggcggg ggacccatcc agatcaccta caactacaac 660
   tacggcgcg cgagcggcat cggctccgac ctgctcaaca acccgacct ggtggcgctc 720
20 gacgccaatc tccttcaaga cggcgttctg gttctggatg acgcccagct cgcccaagcc 780
   gtcgtgccac gcggtgatca ccggccagtg gacgcgctcc gccgacgacc aggcggcggg 840
   cgcgcttccg ggctacggcg agatcaccaa catcatcaac ggcggtgtgg agtgcgggca 900
   cggcgcgga cacaaggtgg ccgaccgat cgggttctac aagcgctact gcgacatgct 960
   gggcgtcagc tatggcgata acctggattg ctacaaccag aggcctacc cgcttctcta 1020
25 gttgatattt gatccgagca gacgaataaa atacaatgca cacgagattg tgagactcga 1080
   gaaaacatat actacctctg aattttaata catatctcta aaacaaaaaa aaaaaaaaaa 1140
   aaaatatac 1149

<210> 38
30 <211> 981
   <212> DNA
   <213> Oryza sativa

<220>
35 <221> misc_feature
   <223> TC84300 (PRO0151)

<400> 38
40 aagaggcaag agcatccgta ttaaccagcc ttttgagact tgagagtgtg tgtgactcga 60
   tccagcgtag tttcagttcg tgtgttggtg agtgattcca gccaaagttg cgatggcttc 120
   tcagcaggaa cgggctagct accacgcccg cgagaccaag gcccgcgccg aggagaagac 180
   gggcgcatg atgggcacgg cgcaggagaa ggcgcgggag gccaaaggaca cggcgctcca 240
   cggcgcgggg cgcgcgatgg gcaggggaca cggcgccaag gaggcgacca aggagaaggc 300
   gtacgagacc aaggacgcga ccaaggagaa ggcgtagcag gcaaaggacg cggcctccga 360
   cgccaccggc cgcgccatgg acaaggcccg cggcgcccg ggcgccacga gggacaaggc 420
45 gtacgatgcc aaggacaggg cggctgacac ggcgagtcg gccgcccacc gcgcccgcga 480
   cggcgccggg cagaccggga gctacattgg acagaccgcc gagggcgcca agcagaaagc 540
   gccggcgccc gcgcagtacg ccaaggagac cgcgatcgcc ggcaaggaca agaccggcgc 600
   cgtgctccag caggcagggg agcagtgtaa gagcgtggcg gtgggggcga aggacgcggt 660
   gatgtacacg ctcggtatgt caggcgataa caagaacaac gccgctgccg gcaaggacac 720
   cagcacctac aagcctggaa ctgggagtga ctaccagtaa tacgtagtaa gaagcatgtg 780
50 tcgtcttttg cactgatgcc aaagtgtacg tgttgatcc tcttttttaa gtttcagctc 840
   gacttcgacg tgttcggtgt cacactttgg tttttcagtt gtgctcaact gttcatgttt 900
   ctggttccat ggagggccag tgtggaagtc aatgtttaag ctttcgtttt aaaatctgat 960
   aataaagttg gttaagacct g 981

55 <210> 39
   <211> 1203

```

EP 1 801 223 A2

<212> DNA
 <213> Oryza sativa

<220>
 5 <221> misc_feature
 <223> TC89687 (PRO0169)

<400> 39
 tactctctctc tctcacctcc accatctagc tcactcacac agtctccact cacacgcatt 60
 10 gcagaggaga ggcgacaatg gaggggaagg aggaggacgt gcggctgggg gcgaacaggt 120
 actcggagag gcagccgata gggacggcgg cgagggcggc gggggacgac aaggactaca 180
 aggagccggc gccgggccgc tgttcgagcc aggggagctc aagtcgtggt ctttctaccg 240
 ggccgggacg gccgagttcg tcgccacctt cctcttcttc tacatcacca tcctcaccgt 300
 catgggggtc tccaagtcct cctccaagtg cgccaccgtc ggcatccagg gcacgcgctg 360
 15 gtccttcgga ggcatgatct tcgcgctcgt ctactgcacc gccggcatct ccggaggaca 420
 catcaaccca gcagttactt ttgggctggt cttggccagg aagctgtccc tgaccggggc 480
 catcttctac atagtgatgc aatgcctagg ggcatctgag ggagctggag ttgtgaaggg 540
 cttccagcag ggtctgtaca tgggcaatgg cggtggtgcc aatgtagttg ccagtggcta 600
 caccaagggt gacggtcttg gtgctgagat tgttggcacc ttcatcctgg tctacaccgt 660
 20 cttctcagcc actgatgcca agaggaatgc cagggactca catgttcta tccttgcccc 720
 actgccaatg ggttttgcgg tgttctggtt ccacctggcc accatcccca tcaccggtag 780
 tggcatcaac ccagccagga gccttggcgc tgccatcatc tacaacaagg accatgcctg 840
 gaatgaccat tggatcttct gggttggtcc cttcgttggc gctgccctgg ctgccatcta 900
 ccaccagggt atcatcaggg cgatcccatc caagagcagg tcttaagccc cgcccgccg 960
 ctgcgcagcc gacgacatgc aacgcaatcg tgatgtcctg tttcccgccg gctactgctg 1020
 25 cgcacatctg gattccctct atctctagtc cccaagatgt ttttctatc tgaaccctga 1080
 acaactcaat cgtgtaatcc agtactcagt cactgtatgt ttttatgtga tggagatctt 1140
 aattcttaag ttatcatctc tgttgctgga aatccggtt cctcttctg catgaaccgc 1200
 gcc 1203

30 <210> 40
 <211> 964
 <212> DNA
 <213> Oryza sativa

<220>
 35 <221> misc_feature
 <223> TC89846 (PRO0170)

<400> 40
 40 cccacggttc cgcccacggt ccgcccacgg tccgcttctc ttctctggtg gtgtgggtgt 60
 gtccctgtct cccctctctc tcctcctctc ctttccctc ctctcttccc ccctctcaca 120
 agagagagag cgccagactc tccccagggt aggattcagc catgaagggg gccaaatcca 180
 agggcgccgc caagcccagc gccaaagtgg ctgtgaagag taagggcgcg gagaagcccg 240
 ccgccaaggg caggaagggg aaggccggca aggaccccaa caagcccaag agggctccct 300
 ccgctttctt cgtttttatg gaggaattcc gtaaggagt caaggagaag aaccccaaga 360
 45 ataaatctgt cgctgctgta ggaaaagcag ccggtgatag gtggaaatcc ctgaccgaag 420
 cggacaaggc tcctatgta gccaaaggcca acaagctcaa ggccgagtag aacaaggcca 480
 ttgctgccta caacaagggc gagagcactg ccaagaaggc acccgccaag gaggaagagg 540
 aggacgacga ggaggaatct gacaagtcca agtccgaggt caatgatgag gatgacgacg 600
 agggcagcga agaggatgaa gacgatgacg agtgagcctt ccagtggaca agatgggagc 660
 50 agcaagacgc taaggggcggc gggcgtccta aggagcctat ccatcatcat catcgtctac 720
 tagaattatt cagtttcact tcacatcgtg atgttttact ttttctctcg tcctataaacg 780
 gatagcgctc cttgttggcg ccaactggtg gtgttgtggt gcagccaatg tcttgtctcc 840
 accgtcaatg atccgcttgt acctagatta ctctttccat tgtcatcggc taacattgtg 900
 ataatatcag tttcggtatg ttatgattaaa ttgtttctaa ttccgctggt ttcttcttcc 960
 ttgc 964

55

EP 1 801 223 A2

```

<210> 41
<211> 1542
<212> DNA
<213> Oryza sativa

5
<220>
<221> misc_feature
<223> TC82935 (PRO0171)

10
<400> 41
cacacctcac acctcaccac catcacctcc tctctctcct cctcttctctc cgcgcgcgcg 60
agatccaggg agagggagag ggagagatca tggcggggac ggtgacggtg ccgtcggcgt 120
cggtgccgctc gacgccgctg ctcaaggacg agctggacat cgtgatcccg acgatccgca 180
acctggactt cctggagatg tggcggccct tcttccagcc ctaccacctc atcatcgtgc 240
15 aggcggcgca cccgaccaag accatccgcg tccccgaggg cttcgactac gagctctaca 300
accgcaacga catcaaccgg atcctcggcc ccaaggcctc ctgcatctcc ttcaaggact 360
ccgcatgccg ctgcttcggc tacatggctt ccaagaagaa gtacgtcttc accatcgacg 420
acgactgctt cgttgccaaag gacccatctg gcaaggacat caatgctctt gagcagcaca 480
tcaagaacct cctcagcccc tccaccccg tcttcttcaa caccttgat gatccctacc 540
gcgaaggcgc tgactttgtc cgtggttacc ctttcagcct caggaggagg gccaagactg 600
20 ctgtctctca cggcctgtgg cttaacatcc ctgactatga tgctcctact cagatgggtca 660
agcctcgtga gaggaactcc aggtatgttg atgctgtcat gactgtgccc aagggaacct 720
tgttcccat gtgtggcatg aaccttgctt ttgaccgtga tctcatcggt cctgcaatgt 780
actttggtct catgggtgat ggccagccta ttggtcgcta cgacgacatg tgggctggat 840
ggtgcatgaa ggtcatctgt gaccacctga gcctgggagt gaagactgga ctgccgtaca 900
25 tctggcacag caaggctagc aaccccttcg tgaacttgaa gaaggaaatc aagggcatct 960
tctggcagga ggacatcatc cccttcttcc agaacgccac catccccaag gagtgcgaca 1020
ccgtccagaa gtgctacctc tccctcgccg agcagggtcag ggagaagctc ggcaagatcg 1080
acccctactt cgtcaagctt gccgatgcc a ttgtcacctg gatcgaggcc tgggatgagc 1140
tgaacccctc gactgctgct gtcgagaacg gcaaggccaa gtagattgat cctgggagct 1200
30 tgtgtgtcgc aggatggaaa gtacccttta agtgaaagtg ttgctgtggc ctaggccccc 1260
tagatatagc tctttttgag atgaaggag agattactta agcaacttta taattctttg 1320
ttgttatgct ggttcttttg tagctggaaa aggattttgt atcatcgttt acataattca 1380
agacaataat aattttatca tgtaattttg atagtcgtgc tttggttgct aaatggtggt 1440
attgtattta ataacccttg caaatcacta tactgtttgg ttgttctgag aattgtatgc 1500
35 actaccatat tatatttcta aatcatttcg taggcattat gg 1542

<210> 42
<211> 1432
<212> DNA
<213> Oryza sativa

40
<220>
<221> misc_feature
<223> TC82977 (PRO0173)

45
<220>
<221> misc_feature
<222> (1429)..(1429)
<223> n = any nucleotide

50
<400> 42
aaaagagcag cgctgcctct cctcctccct aacccctacg cttccagaac cttctcgaag 60
ctcccgcctc cccccccctt ccgtcccaat ggcaaggaa ccgatgcgcg tgctcgtcac 120
cggcgccgca ggacaaattg gatatgctct tgtcccatg attgctaggg gtgtgatggt 180
gggtgctgac cagcctgtta ttctacacat gcttgacatt ccaccagcta ctgaatctct 240
taatggcctt aagatggagc tggttgatgc tgcatttcct cttttgaagg gaattgtcgc 300
55 aacaactgat gttgtggagg cctgcactgg tgtgaatggt gcggttatgg ttggtgggtt 360
ccccaggaag gagggaatgg aaaggaagga tgttatgtca aaaaatgtct ccatctacaa 420

```

EP 1 801 223 A2

```

    atcccaagct tctgctcttg aggctcatgc agcccctaac tgcaagggttc tggtagttgc      480
    caatccagca aacaccaacg ctctcatctt aaaagaattc gctccatcca tccctgagaa      540
    gaacattact tgccctcacc gtcttgacca caacagggca ctgggccaga tctctgaaaa      600
    acttaatgtc caagttactg atgtgaagaa tgcgatcatc tggggcaacc actcatccac      660
5    ccagtagcct gatgttaacc acgccactgt gaagactccc agtggagaga agcctgtcag      720
    ggaactcggt gctgatgatg agtgggttaa tacggaattc atctctaccg tccagcagcg      780
    tggtgccgcc atcatcaagg cgaggaagca atccagtgcc ctatctgctg ccagctctgc      840
    atgcgatcac attcgtgact gggttcttgg cactcctgag ggaacatttg tctccatggg      900
    tgtgtactct gatggttcgt atgggtgtcc tgctggtctg atctactcgt tcccagtaac      960
10   atcgagtggg ggcgaatgga cgattgttca gggctctccc atcgacgagt tctcaaggaa     1020
    gaagatggac gcgactgccc aggagctgtc ggaggagaag acgctcgctt actcatgcct     1080
    caactaaaac taagcaatac ccagagggac agatagttag cgattgcccg ctcccggtgt     1140
    tttgaataaa agagactttt aagttccatc acatagaaac tgtttatctc agaccgctgc     1200
    acatcgcgag atgtggagcg cagatgccgt tgctggtttt actccagtgt gtattgaggc     1260
15   tttgtactag ctcccctttt tttgcctggt gattcgcagg acatttgctg aaaacattga     1320
    acccatttga catctgatgg aatcatggac cagtagcaag tacatttttg cgaaagcata     1380
    atctgcacgc ggcttgggct ggtggttgaa ctttctgcca catggcccnt gg              1432

<210> 43
<211> 659
20  <212> DNA
    <213> Oryza sativa

<220>
<221> misc_feature
25  <223> TC83646 (PRO0175)

<400> 43
    gctaagttag cttagccactg atcagaagaa cacctcgatc tctgagagtg ttttttcagc      60
    tttagcttaa gcaggatgga gcaccagggg cagcacggcc acgtgaccag ccgcgtcgac     120
30   gagtacggca acccggtcgg caccggcgcc ggacacggcc agatgggcac cgccggcatg     180
    gggacgcacg gcaccgccgg caccggcgcc ggccagttcc agccgatgag ggaggagcac     240
    aagaccggcg cgttcctgca acgctccggc agctccagct caagctcgtc tgaggatgat     300
    ggaatgggag ggaggaggaa gaaggggagc aaggagaaga tcaaggagaa gctccccggc     360
    ggcaacaagg gcgagcagca gcattgccat ggcggcaccg gcaccggcac cggcaccggc     420
35   accggaaccg gcggcgccca cgggcagcag ggccacggca ccgggatgac caccggcacc     480
    accggcgcac accggcaccac caccaccgac accggcgaga agaagggcac catggacaag     540
    atcaaggaga agctgcccgg ccagcactga gctcgacaca ccaccacacc atgtgtctgc     600
    gcccccgggc accgcccgca cgtcaccttc ctgaataata agatgagcta accgagcgc     659

<210> 44
40  <211> 1310
    <212> DNA
    <213> Oryza sativa

<220>
<221> misc_feature
45  <223> TC90619 (PRO0177)

<400> 44
    ggaccagcga gcaaccagcc ccccgccccc aatggcggca gagcagcttt gccaccgct      60
    gccgcttttg cccacctctc ctccgattaa tcccctcccc tctcttctct cccacttctc     120
50   cgctcctctc tctcccctc gccgacccta cctactcgcg ccgcccgggt cgattgggc      180
    ggcaaacgga ggggggggta accctgatgg agcagtacga gaaggaggag aagattgggg      240
    agggcacgta cggggtgggt tacagggcgc gggacaaggc caccaacgag acgatcgcg      300
    tcaagaagat ccggcttgag caggaggatg agggcgctcc ctccaccgca atccgcgaga     360
    tctcgctcct caaggagatg catcacggca acatcgtcag gttacacgat gttatccaca     420
55   gtgagaagcg catatatctt gtctttgagt atctggatct ggacctaaag aagttcatgg     480
    actcttgtcc agagtttgcg aaaaacccca ctttaattaa gtcatatctc tatcagatac     540

```

EP 1 801 223 A2

```

tccgcggcgt tgcctactgt cattctcata gagttcttca tcgagatttg aaacctcaga      600
atattattgat agatcggcgt actaatgcac tgaagcttgc agacttttgt ttagccaggg      660
cattttggaat tctgtgccgc acgtttactc acgagggtgt aaccttgttg tatagagctc      720
cagagatcct tcttgatca aggcagtatt ctacaccagt tgatatgtgg tcagttgggt      780
5  gtatctttgc agaaatggtg aaccagaaac cactgttccc tggtgattct gagattgatg      840
aattatttaa gatattcagg gtactaggaa ctccaaatga acaaagttgg ccaggagtta      900
gctcattacc tgactacaag tctgctttcc ccaagtggca agcacaggat cttgcaacta      960
ttgtccctac tcttgaccct gctggtttgg accttctctc taaaatgctt cggtagcagc     1020
caaacaaaag gatcacagct agacaggctc ttgagcatga atacttcaag gaccttgaga     1080
10  tggtagaatg accctgctat ggctttacat tggattggca tatgtatggg ctgggctcct     1140
catttcattc cttctgtgaa cgctgtgccc ttcgtttggg catttttgtc attcagctgg     1200
atatttcaaa tcttgtgtgt ttgatatgta ttcaggaacg ctaaatagat caccgtcttg     1260
gtctctatatt gttcagagta aatatcttcc aatgctgcct ttcagtttcc     1310

<210> 45
<211> 55
<212> DNA
<213> Artificial sequence

<220>
20  <223> prm3780

<400> 45
ggggacaagt ttgtacaaaa aagcaggctt cgacgctact caagtgggtg gaggc      55

25  <210> 46
<211> 55
<212> DNA
<213> Artificial sequence

30  <220>
<223> prm2768

<400> 46
ggggacaagt ttgtacaaaa aagcaggctc ccgatttagt agaccacatt ttggc      55

35  <210> 47
<211> 54
<212> DNA
<213> Artificial sequence

40  <220>
<223> prm2420

<400> 47
ggggacaagt ttgtacaaaa aagcaggcta tgccatcgag tgggtgtgccg atac      54

45  <210> 48
<211> 54
<212> DNA
<213> Artificial sequence

50  <220>
<223> prm2853

<400> 48
ggggacaagt ttgtacaaaa aagcaggctt ctcttctgaa gctgaagccc tgcg      54
55

```

EP 1 801 223 A2

<210> 49
<211> 53
<212> DNA
5 <213> Artificial sequence

<220>
<223> prm2426

10 <400> 49
ggggacaagt ttgtacaaaa aagcaggcta aaaccaccga gggacctgat ctg 53

<210> 50
<211> 55
<212> DNA
15 <213> Artificial sequence

<220>
<223> prm2855

20 <400> 50
ggggacaagt ttgtacaaaa aagcaggctc ctagctatat gcagagggtg acagg 55

<210> 51
<211> 53
<212> DNA
25 <213> Artificial sequence

<220>
<223> prm3025

30 <400> 51
ggggacaagt ttgtacaaaa aagcaggcta tgggtgccatg tcaataagac atc 53

<210> 52
<211> 56
<212> DNA
35 <213> Artificial sequence

<220>
<223> prm3029

40 <400> 52
ggggacaagt ttgtacaaaa aagcaggctg tttttctatg aaccggtcat taaacc 56

<210> 53
<211> 55
<212> DNA
45 <213> Artificial sequence

<220>
<223> prm3061

50 <400> 53
ggggacaagt ttgtacaaaa aagcaggctc ctgatggatg atgaatcact gatcg 55

<210> 54
<211> 57
<212> DNA
55

EP 1 801 223 A2

<213> Artificial sequence

<220>

5 <223> prm3031

<400> 54
ggggacaagt ttgtacaaaa aagcaggctt cgtaaagttt gatgatttct gatgacc 57

<210> 55
10 <211> 53
<212> DNA
<213> Artificial sequence

<220>

15 <223> prm3051

<400> 55
ggggaccact ttgtacaaga aagctgggtg ccgccgctcg ctgcttctgt tcg 53

<210> 56
20 <211> 58
<212> DNA
<213> Artificial sequence

<220>

25 <223> prm3592

<400> 56
ggggacaagt ttgtacaaaa aagcaggctc gtgttcatgt tcgcatttag gattggac 58

<210> 57
30 <211> 55
<212> DNA
<213> Artificial sequence

<220>

35 <223> prm5131

<400> 57
ggggacaagt ttgtacaaaa aagcaggctc agatgccaca gtatggtgta ccacc 55

<210> 58
40 <211> 56
<212> DNA
<213> Artificial sequence

<220>

45 <223> prm3782

<400> 58
ggggacaagt ttgtacaaaa aagcaggctt tgcagttgtg accaagtaag ctgagc 56

<210> 59
50 <211> 54
<212> DNA
<213> Artificial sequence

<220>

55 <223> prm2844

EP 1 801 223 A2

<400> 59
ggggacaagt ttgtacaaaa aagcaggctt ttggcgcggg gcagaagagt ggac 54

5 <210> 60
<211> 57
<212> DNA
<213> Artificial sequence

10 <220>
<223> prm2973

<400> 60
ggggacaagt ttgtacaaaa aagcaggctg cttgagtcac agggagaaaa caaatcg 57

15 <210> 61
<211> 53
<212> DNA
<213> Artificial sequence

20 <220>
<223> prm3770

<400> 61
ggggacaagt ttgtacaaaa aagcaggctc gtcctccttt tgtaacggct cgc 53

25 <210> 62
<211> 56
<212> DNA
<213> Artificial sequence

30 <220>
<223> prm3772

<400> 62
ggggacaagt ttgtacaaaa aagcaggctc atggggctaa tgtagatgct cactgc 56

35 <210> 63
<211> 53
<212> DNA
<213> Artificial sequence

40 <220>
<223> prm3774

<400> 63
ggggacaagt ttgtacaaaa aagcaggctt agtaccattc ttccctcgtg agc 53

45 <210> 64
<211> 53
<212> DNA
<213> Artificial sequence

50 <220>
<223> prm3776

<400> 64
ggggacaagt ttgtacaaaa aagcaggctg tttgggttggg gaccgcaatt tgc 53

55

EP 1 801 223 A2

<210> 65
<211> 55
<212> DNA
<213> Artificial sequence
5
<220>
<223> prm3800
<400> 65
10 ggggacaagt ttgtacaaaa aagcaggctg tcaccaccgt catgtacgag gctgc 55
<210> 66
<211> 55
<212> DNA
15 <213> Artificial sequence
<220>
<223> prm5135
<400> 66
20 ggggacaagt ttgtacaaaa aagcaggctc agacacctag aatatagaca ttccc 55
<210> 67
<211> 55
<212> DNA
25 <213> Artificial sequence
<220>
<223> prm3781
<400> 67
30 ggggaccact ttgtacaaga aagctgggtg atcacaagcg cagctaataca ctagc 55
<210> 68
<211> 57
<212> DNA
35 <213> Artificial sequence
<220>
<223> prm2769
<400> 68
40 ggggaccact ttgtacaaga aagctgggtc gtgtagaaaa tcttaaccgcg aaaatcg 57
<210> 69
<211> 55
<212> DNA
45 <213> Artificial sequence
<220>
<223> prm2421
<400> 69
50 ggggaccact ttgtacaaga aagctgggtg gtgaggtgcc ggggaagcga cgttg 55
<210> 70
<211> 54
55 <212> DNA
<213> Artificial sequence

EP 1 801 223 A2

<220>
<223> prm2854

5 <400> 70
ggggaccact ttgtacaaga aagctggggtt tcttctttcc cttggaacta accg 54

<210> 71
<211> 54
10 <212> DNA
<213> Artificial sequence

<220>
<223> prm2427

15 <400> 71
ggggaccact ttgtacaaga aagctggggtt gtcgctttta tttggcttgg tgtg 54

<210> 72
<211> 56
20 <212> DNA
<213> Artificial sequence

<220>
<223> prm2856

25 <400> 72
ggggaccact ttgtacaaga aagctggggtc tctagctcga tctctcttgc aaaagc 56

<210> 73
<211> 49
30 <212> DNA
<213> Artificial sequence

<220>
<223> prm3026

35 <400> 73
ggggaccact ttgtacaaga aagctggggtg gcgatgagat cttctctcg 49

<210> 74
<211> 59
40 <212> DNA
<213> Artificial sequence

<220>
<223> prm3030

45 <400> 74
ggggaccact ttgtacaaga aagctggggtt tttgtaggat tctactacta tgcttcaac 59

<210> 75
<211> 62
50 <212> DNA
<213> Artificial sequence

<220>
<223> prm3062

55

EP 1 801 223 A2

<400> 75
ggggaccact ttgtacaaga aagctgggta ttgtgtaaat atttctattg tccagtaatc 60
ac 62

5 <210> 76
<211> 54
<212> DNA
<213> Artificial sequence

10 <220>
<223> prm3032

<400> 76
ggggaccact ttgtacaaga aagctgggtg atggcagagt taattagcaa acgc 54

15 <210> 77
<211> 50
<212> DNA
<213> Artificial sequence

20 <220>
<223> prm3052

<400> 77
ggggacaagt ttgtacaaaa aagcaggctc taagggcagc agccattggg 50

25 <210> 78
<211> 60
<212> DNA
<213> Artificial sequence

30 <220>
<223> prm3049

<400> 78
ggggaccact ttgtacaaga aagctgggtg gcggcggcgg cgycggcggc ggctgggtct 60

35 <210> 79
<211> 54
<212> DNA
<213> Artificial sequence

40 <220>
<223> prm2195

<400> 79
ggggaccact ttgtacaaga aagctgggtc ggcttagaga ggggaggaag cgaa 54

45 <210> 80
<211> 58
<212> DNA
<213> Artificial sequence

50 <220>
<223> prm2197

<400> 80
ggggaccact ttgtacaaga aagctgggtt ggtgtgagt tttgagttg gagtgagc 58

55

EP 1 801 223 A2

<210> 81
<211> 57
<212> DNA
<213> Artificial sequence
5

<220>
<223> prm2845

<400> 81
10 ggggaccact ttgtacaaga aagctggggtc ggcaatgtga tgcaatgcaa attaagc 57

<210> 82
<211> 55
<212> DNA
15 <213> Artificial sequence

<220>
<223> prm2974

<400> 82
20 ggggaccact ttgtacaaga aagctggggtc gcaaacttgg ctggaatcac tcacc 55

<210> 83
<211> 54
<212> DNA
25 <213> Artificial sequence

<220>
<223> prm3771

<400> 83
30 ggggaccact ttgtacaaga aagctggggtt gtcgcctctc ctctgcaatg cgtg 54

<210> 84
<211> 52
<212> DNA
35 <213> Artificial sequence

<220>
<223> prm3773

<400> 84
40 ggggaccact ttgtacaaga aagctgggtg gctgaatcct gcgagaaggg cg 52

<210> 85
<211> 54
<212> DNA
45 <213> Artificial sequence

<220>
<223> prm3775

<400> 85
50 ggggaccact ttgtacaaga aagctgggtg atctctccct ctccctctcc ctgg 54

<210> 86
<211> 52
55 <212> DNA
<213> Artificial sequence

EP 1 801 223 A2

<220>
 <223> prm3777
 5 <400> 86
 ggggaccact ttgtacaaga aagctggggtt ggagcggaag ggggggggga gc 52
 <210> 87
 <211> 57
 10 <212> DNA
 <213> Artificial sequence
 <220>
 <223> prm3801
 15 <400> 87
 ggggaccact ttgtacaaga aagctggggtc actctcagag atcgagggtgt tcttctg 57
 <210> 88
 20 <211> 52
 <212> DNA
 <213> Artificial sequence
 <220>
 25 <223> prm5136
 <400> 88
 ggggaccact ttgtacaaga aagctggggtc gcccgagct cgcccccgtc cg 52

30

Claims

- 35 1. An isolated promoter capable of driving and/or regulating expression, comprising:
 (a) an isolated nucleic acid as given in any one of SEQ ID NO: 5, SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22 or the complement of any one of the aforementioned sequences; or
 40 (b) an isolated nucleic acid having at least 90% sequence identity with any of the DNA sequences as given in any one of SEQ ID NO: 5, SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22; or
 45 (c) an isolated nucleic acid specifically hybridizing under stringent conditions with any of the DNA sequences as given in any one of SEQ ID NO: 5, SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22; or
 50 (d) an isolated nucleic acid as defined in any one of (a) to (c), which is interrupted by an intervening sequence; or
 (e) a fragment of any of the nucleic acids as defined in (a) to (d), which fragment is capable of driving and/or regulating expression.
 55 2. A promoter according to claim 1, which is a hybrid promoter comprising at least one part of a promoter as defined in claim 1 and further comprising another part of a promoter.
 3. A genetic construct comprising:

EP 1 801 223 A2

- (a) An isolated promoter as defined in claim 1 or 2; and
- (b) a heterologous nucleic acid sequence operably linked to said promoter of (a); and optionally
- (c) a 3' transcription terminator.

- 5 4. An expression cassette comprising a genetic construct as defined in claim 3.
5. A transformation vector comprising a genetic construct as defined in claim 3.
- 10 6. An expression vector comprising a genetic construct as defined in claim 3.
7. A host cell comprising an isolated promoter as defined in claim 1 or 2, or genetic construct as defined in claim 3, or an expression cassette as defined in claim 4, or a transformation vector as defined in claim 5, or an expression vector as defined in claim 6.
- 15 8. Host cell according to claim 7, selected from a bacteria, algae, fungi, yeast, plant, insect and animal host cell.
9. A transgenic plant cell comprising an isolated promoter as defined in claim 1 or 2, or a genetic construct as defined in claim 3, or an expression cassette as defined in claim 4 or a transformation vector as defined in claim 5 or an expression vector as defined in claim 6.
- 20 10. Transgenic plant cell according to claim 9, which is a monocot plant cell.
11. Transgenic plant cell according to claim 10, which is a dicot plant cell.
- 25 12. A transgenic plant comprising a transgenic plant cell as defined in claim 10 or 11.
13. A transgenic plant according to claim 12, wherein said plant is selected from rice, maize, wheat, barley, millet, oats, rye, sorghum, soybean, sunflower, canola, sugarcane, alfalfa, bean, pea, flax, lupinus, rapeseed, tobacco, tomato, potato, squash, papaya, poplar and cotton.
- 30 14. Plant part, preferably a harvestable part, a propagule or progeny of a plant as defined in claim 13 or 14.
15. Method for driving and/or regulating expression of a nucleic acid in a plant or plant cell, comprising:
- 35 (a) Operably linking said nucleic acid to any one of the isolated nucleic acids as defined in claim 1, and
- (b) Introducing the resultant genetic construct into a plant or plant cell.
16. Method according to claim 15, wherein said expression is constitutive or tissue-specific.
- 40 17. Method for the production of a transgenic plant, comprising:
- (a) Introducing into a plant cell an isolated promoter as defined in claim 1 or 2, or a genetic construct as defined in claim 3, or an expression cassette as defined in claim 4, or a transformation vector as defined in claim 5 or an expression vector as defined in claim 6, and
- 45 (b) Cultivating said plant cell under conditions promoting plant growth.
18. Use of any of the isolated nucleic acids as defined in claim 1 to drive and/or regulate expression of an operably linked nucleic acid.
- 50
- 55

EP 1 801 223 A2

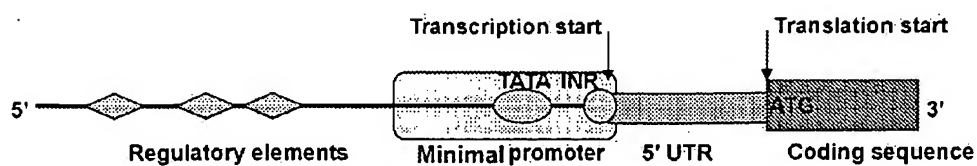


FIGURE 1

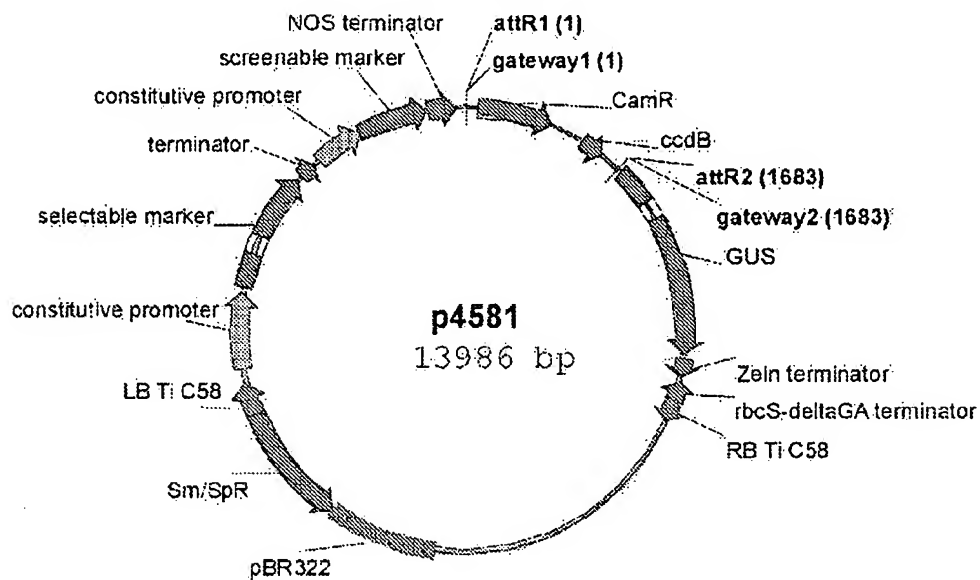


FIGURE 2

PRO0110 RCc3

C plant

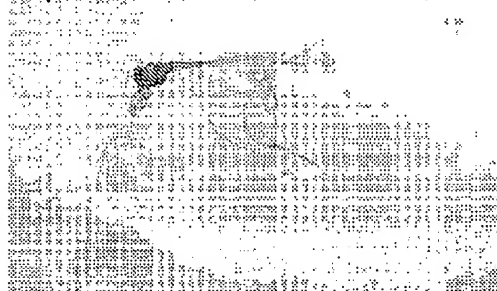


FIGURE 3

EP 1 801 223 A2

PRO0005 putative beta-amylase



FIGURE 4

PRO0009 putative cellulose synthase

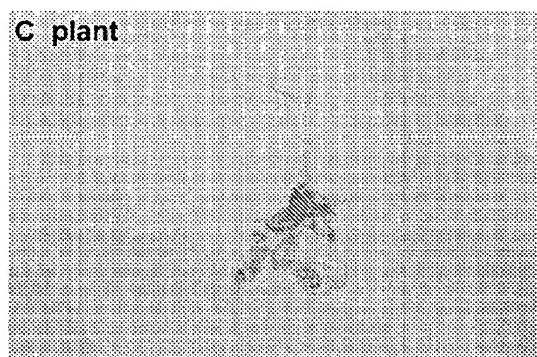


FIGURE 5

PRO058 proteinase inhibitor Rgpi9

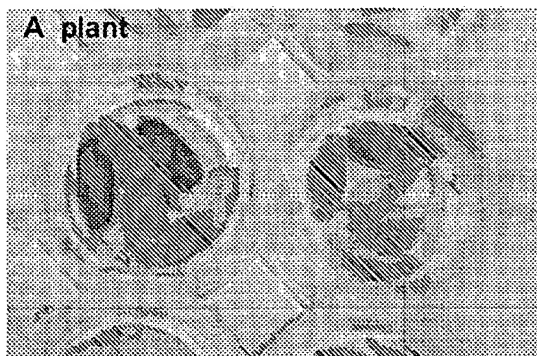


FIGURE 6

EP 1 801 223 A2

PRO061 beta-expansin EXPB9

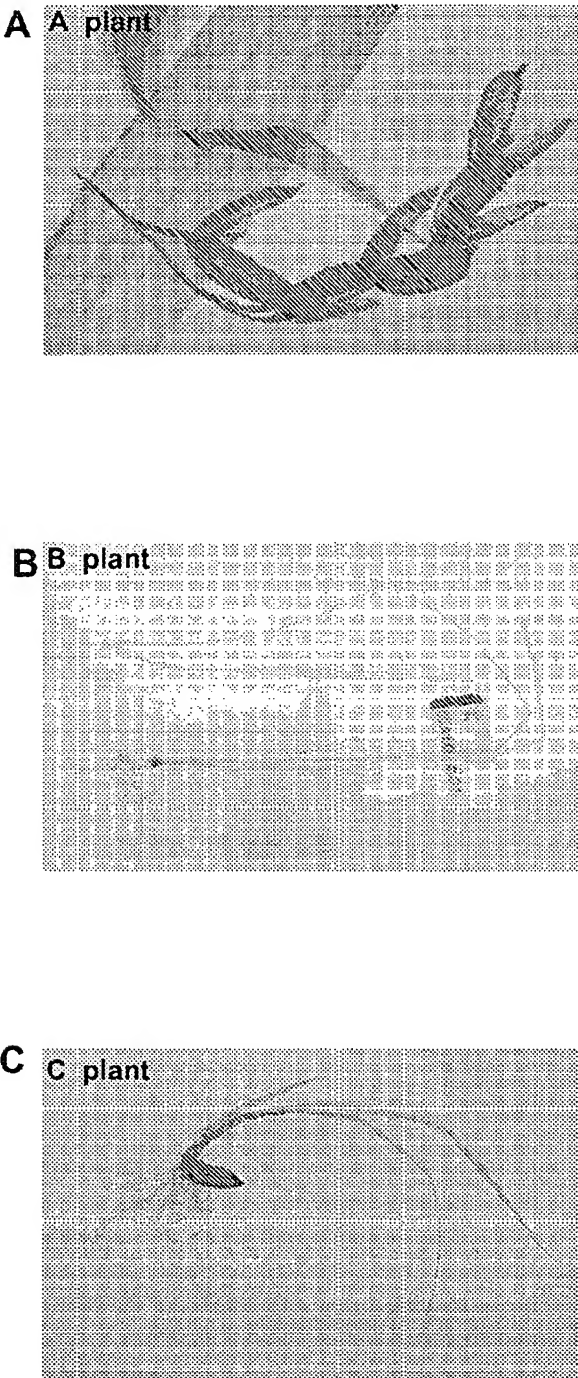
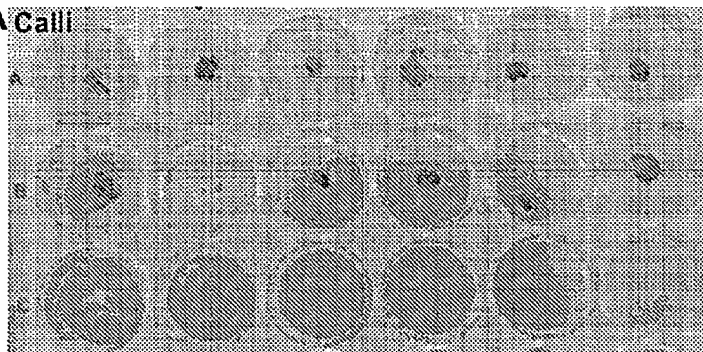
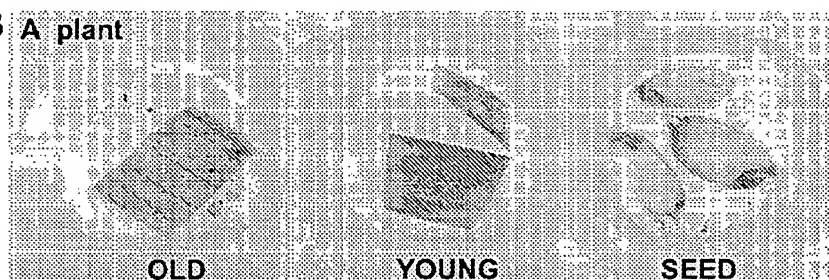
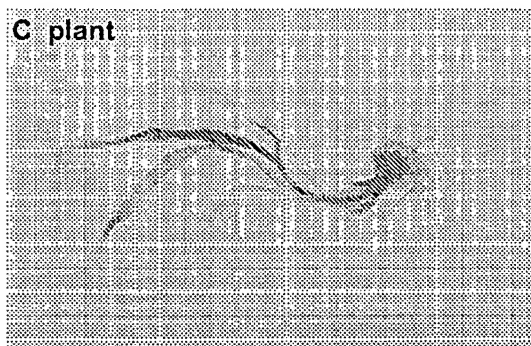


FIGURE 7

EP 1 801 223 A2**PRO0063 structural protein****A calli****B A plant****FIGURE 8****PRO0081 putative caffeoyl CoA 3-O-methyltransferase****C plant****FIGURE 9**

EP 1 801 223 A2

PRO0091 prolamin RP5

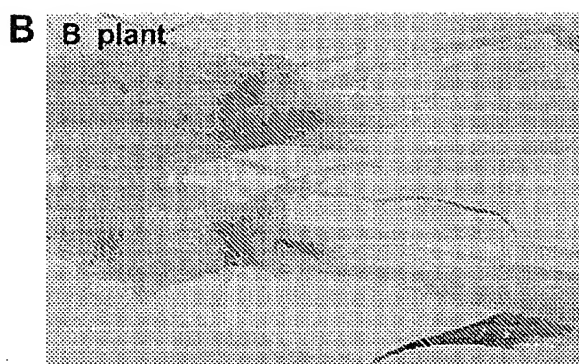
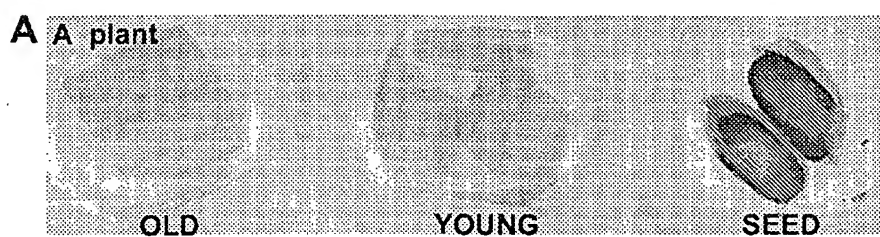


FIGURE 10

PRO0095 putative methionine aminopeptidase

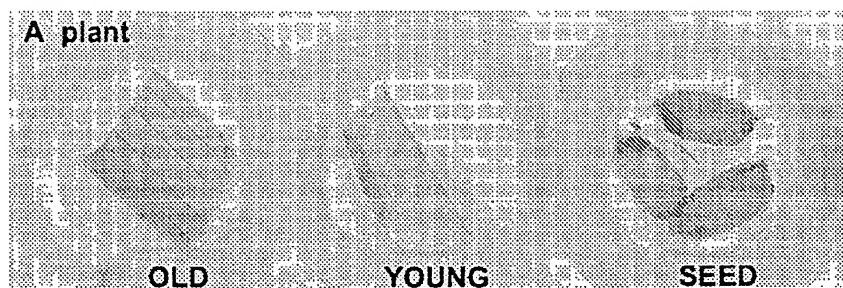


FIGURE 11

EP 1 801 223 A2

PRO0111 uclacyanin 3-like protein

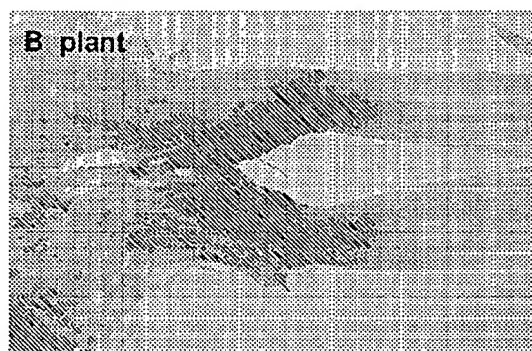


FIGURE 12

PRO0116 26S proteasome regulatory particle non-ATPase subunit 11

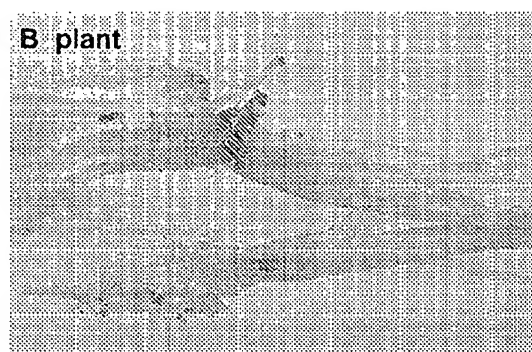


FIGURE 13

PRO0117 putative 40S ribosomal protein

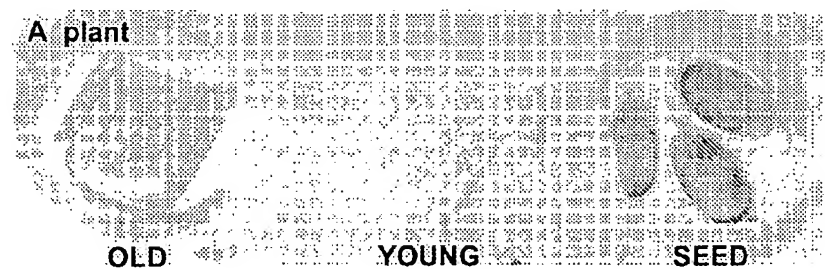


FIGURE 14

EP 1 801 223 A2

PRO0122 chlorophyll a/b binding protein precursor (Cab27)

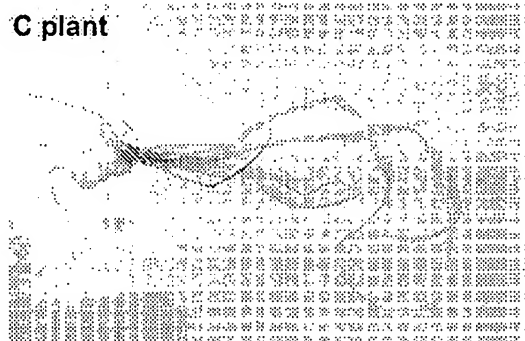


FIGURE 15

PRO0123 putative protochlorophyllide reductase

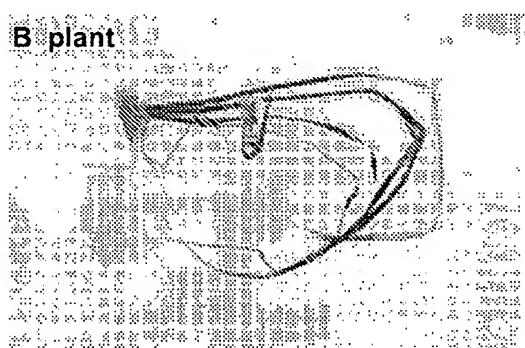


FIGURE 16

PRO0133 chitinase Cht-3

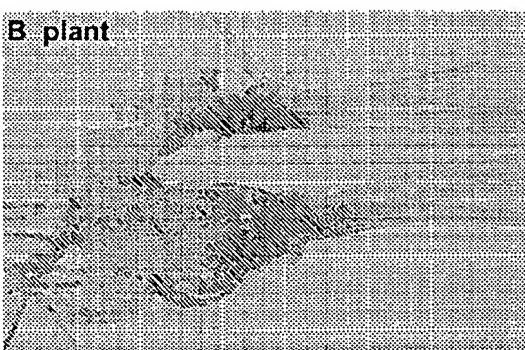
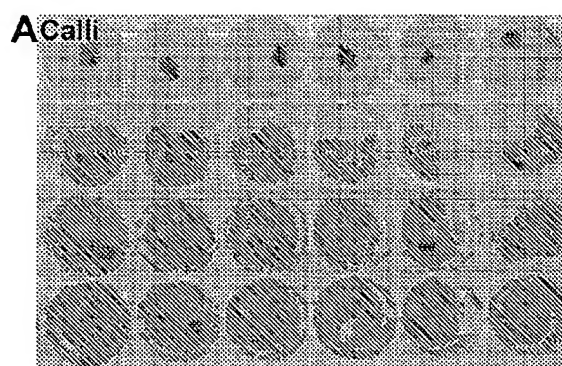


FIGURE 17

EP 1 801 223 A2

PRO0151 WSI18



B Seed

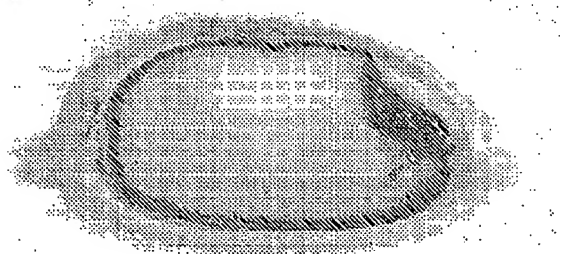


FIGURE 18

PRO0169 aquaporine

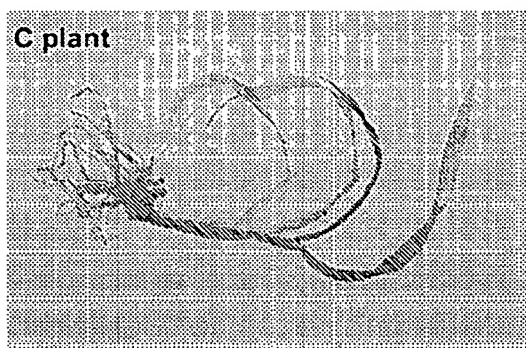
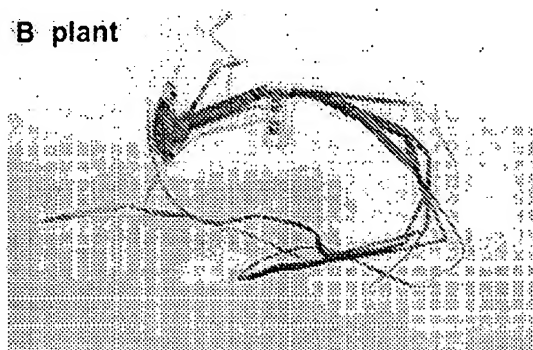


FIGURE 19

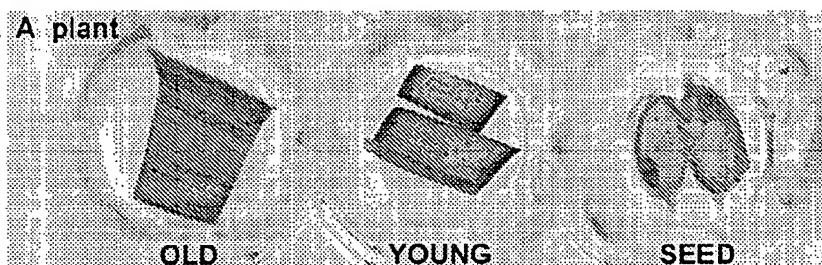
EP 1 801 223 A2

PRO0170 high mobility group protein

A B plant



B A plant



C Calli

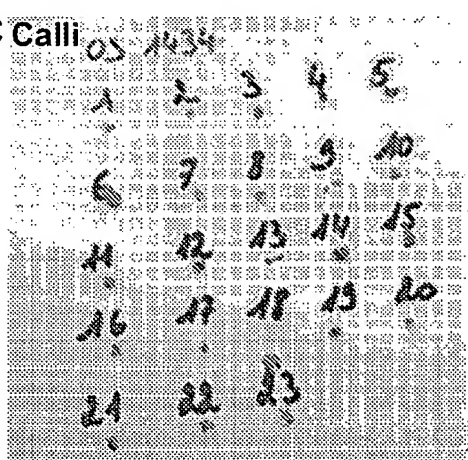


FIGURE 20

EP 1 801 223 A2

PRO0171 reversibly glycosylated protein RGP1

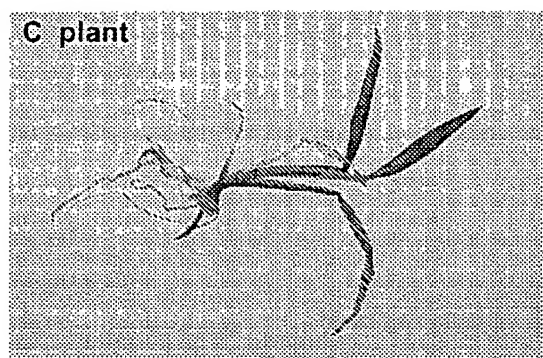


FIGURE 21

PRO0173 cytosolic MDH

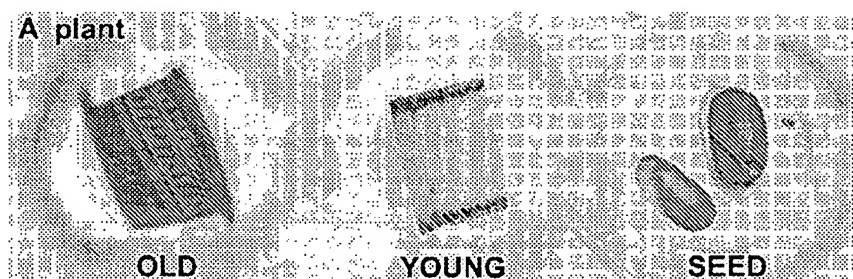


FIGURE 22

EP 1 801 223 A2

PRO0175 RAB21

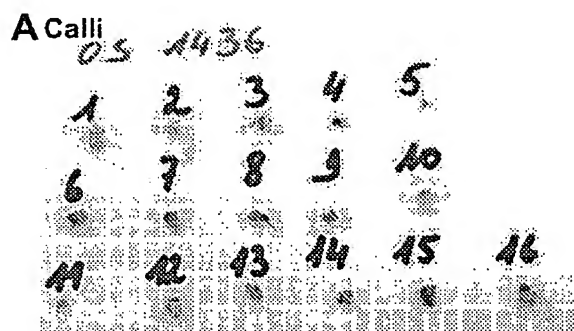
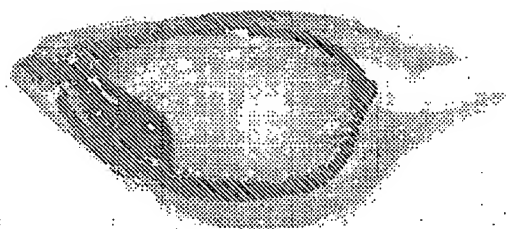
**B Seed**

FIGURE 23

PRO0177 Cdc2-1

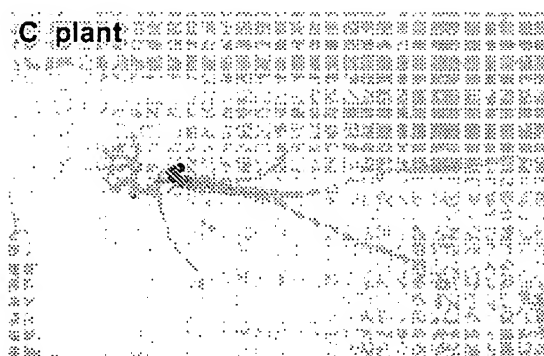


FIGURE 24

EP 1 801 223 A2**REFERENCES CITED IN THE DESCRIPTION**

This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

Patent documents cited in the description

- EP 1198985 A1 [0054]

Non-patent literature cited in the description

- NEEDLEMAN-WUNSCH. *J. Mol. Biol.*, 1970, vol. 48, 443-453 [0009]
- SMITH-WATERMAN. *Advances in Applied Mathematics*, 1981, vol. 2, 482-489 [0009]
- COULSON. *Trends in Biotechnology*, 1994, 76-80 [0010]
- BIRREN et al. *GenomeAnalysis*, 1997, vol. 1, 543 [0010]
- SAMBROOK. *Molecular Cloning: a laboratory manual*. Cold Spring Harbor Laboratory Press, 2001 [0014]
- KRENS, F.A. et al. *Nature*, vol. 296, 72-74 [0053]
- NEGRUTIU I. et al. *Plant Mol. Biol.*, June 1987, vol. 8, 363-373 [0053]
- SHILLITO R.D. et al. *Bio/Technol*, 1985, vol. 3, 1099-1102 [0053]
- CROSSWAY A. et al. *Mol. Gen Genet*, 1986, vol. 202, 179-185 [0053]
- KLEIN T.M. et al. *Nature*, 1987, vol. 327, 70 [0053]
- ALDEMITA ; HODGES. *Planta*, 1996, vol. 199, 612-617 [0054]
- CHAN et al. *Plant Mol. Biol.*, 1993, vol. 22 (3), 491-506 [0054]
- HIEI et al. *Plant J.*, 1994, vol. 6 (2), 271-282 [0054]
- ISHIDA et al. *Nat. Biotechnol.*, June 1996, vol. 14 (6), 745-50 [0054]
- FRAME et al. *Plant Physiol.*, May 2002, vol. 129 (1), 13-22 [0054]